



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179469

TO: Delia Ramirez
Location: 2d74 / 2c70
Art Unit: 1652
Friday, February 17, 2006

Case Serial Number: 10/040018

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

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Jarrell, Noble

179469

From: Ramirez, Delia
Sent: Monday, February 13, 2006 10:22 AM
To: Jarrell, Noble
Subject: 10/041018

Hi,

I would like to request the following *interference* search:

1. SEQ ID NO: 1, 361, 22 and 383 in the nucleic acid databases.
2. nucleotides 10000-10200 of SEQ ID NO:399 in the nucleic acid databases.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Mtbe
Fin 2/17/06
SNA
Compuser SPR
Soul

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:38:14 ; Search time 145.397 Seconds
(without alignments)
2934.525 Million cell updates/sec

Title: US-10-041-018-399_COPY_10000_10200

Perfect score: 201

Sequence: 1 aagaagtagcacattcataa.....catcgctattgcactctgca 201

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US12_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US13_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US14_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US15_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US16_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US17_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US18_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	32.6	16.2	187745	12	US-11-121-086-83	
2	31.2	15.5	581	6	US-09-925-065A-194717	
3	31.2	15.5	613	6	US-09-925-065A-114512	
4	30.8	15.3	581	6	US-09-925-065A-114514	
5	30.8	15.3	613	6	US-09-925-065A-114513	
c	30.8	15.3	638	6	US-09-925-065A-54797	
7	30.4	15.1	583	6	US-09-925-065A-446887	
c	30.2	15.0	458	6	US-09-925-065A-146565	
9	30.2	15.0	520	6	US-09-925-065A-22533	
10	30.2	15.0	520	6	US-09-925-065A-22534	
c	11	30.2	15.0	2072	6	US-09-925-065A-700722
c	12	30.2	15.0	2072	6	US-09-925-065A-700723
c	13	30.2	15.0	2072	6	US-09-925-065A-700724
c	14	30.2	15.0	2072	6	US-09-925-065A-700725
15	30.2	15.0	2722	8	US-10-750-185-25210	
16	30.2	15.0	2722	8	US-10-750-185-25210	
c	17	30	14.9	574	6	US-09-925-065A-195489
c	18	30	14.9	638	6	US-09-925-065A-197353
c	19	29.8	14.8	600	12	US-11-136-527-4276
c	20	29.8	14.8	2505	8	US-10-750-185-26139

c	21	29.8	14.8	2505	8	US-10-750-623-26139
c	22	29.8	14.8	2519	12	US-11-136-527-180
c	23	29.6	14.7	913	8	US-10-750-185-38221
c	24	29.6	14.7	913	8	US-10-750-623-38221
c	25	29.4	14.6	527	6	US-09-925-065A-437898
c	26	29.4	14.6	919	8	US-10-750-185-49248
c	27	29.4	14.6	919	8	US-10-750-623-49248
c	28	29.4	14.6	1137	8	US-10-750-185-35492
c	29	29.4	14.6	1137	8	US-10-750-623-35492
c	30	29.4	14.6	18682	12	US-11-112-908-23
c	31	29.2	14.5	604	6	US-09-925-065A-210001
c	32	29	14.4	600	8	US-10-750-185-20355
c	33	29	14.4	600	8	US-10-750-623-20355
c	34	29	14.4	1027	8	US-10-750-185-38774
c	35	29	14.4	1027	8	US-10-750-623-38774
c	36	29	14.4	2681	12	US-11-239-325-8
c	37	29	14.4	2699	12	US-11-239-325-26
c	38	29	14.4	319608	12	US-11-145-703-1
c	39	28.8	14.3	545	6	US-09-925-065A-24019
c	40	28.8	14.3	578	6	US-09-925-065A-379132
c	41	28.8	14.3	599	6	US-09-925-065A-634390
c	42	28.8	14.3	915	8	US-10-750-185-46586
c	43	28.8	14.3	915	8	US-10-750-623-46586
c	44	28.6	14.2	645	6	US-09-925-065A-165968
c	45	28.4	14.1	578	6	US-09-925-065A-379130

ALIGNMENTS

RESULT 1

US-11-121-086-83
; Sequence 83, Application US/11121086
; Publication No. US20050286459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 83
; LENGTH: 187745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-83

Query Match 16.2%; Score 32.6; DB 12; Length 187745;
Best Local Similarity 60.9%; Pred. No. 9.7;
Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy	8	AGCACATTCATACGACGAGTACGAACTCTTTACACCCCGAGACAGTTGCCCTA	67
Db	53154	AGGACAGATCAACATCGGAGATACAAACTGTCTAAGTACTATACATCTGTTCCATTA	53213
Qy	68	TATCGCTTTTCCCTATCAATAGTTTCT	94
Db	53214	TATCCCTTATCCCAATCCATTACTCT	53240

RESULT 2

US-09-925-065A-194717
; Sequence 194717, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135

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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194717
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-194717

Query Match      15.5%; Score 31.2; DB 6; Length 581;
Best Local Similarity 57.0%; Pred. No. 4.6;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATCGCTTTCCCTATCAATAGTTTCTAA 96
DB 275 CATCCTTAAACTTCCCTGGCCCTGATGCTCTTGTGCGGATCTGTGATTATAGATCCCAA 334

QY 97 CTCATGTCAGTCTTGGGATCACAACTCTTCAGTTGTAC 136
DB 335 GTCTTCCTTTCTTTGTAATACATCCTCATCTGTTCTGC 374

RESULT 3
US-09-925-065A-114512
; Sequence 114512, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114512
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-114512

Query Match      15.5%; Score 31.2; DB 6; Length 613;
Best Local Similarity 57.0%; Pred. No. 4.7;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATCGCTTTCCCTATCAATAGTTTCTAA 96
DB 367 CATCCTTAAACTTCCCTGGCCCTGATGCTCTTGTGCGGATCTGTGATTATAGATCCCAA 426

QY 97 CTCATGTCAGTCTTGGGATCACAACTCTTCAGTTGTAC 136
DB 427 GTCTTCCTTTCTTTGTAATACATCCTCATCTGTTCTGC 466

; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114513
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-114513

Query Match      15.3%; Score 30.8; DB 6; Length 581;
Best Local Similarity 56.0%; Pred. No. 6.2;
Matches 56; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATCGCTTTCCCTATCAATAGTTTCTAA 96
DB 275 CATCCTTAAACTTCCCTGGCCCTGATGCTCTTGTGCGGATCTGTGATTATAGATCCCAA 334

QY 97 CTCATGTCAGTCTTGGGATCACAACTCTTCAGTTGTAC 136
DB 335 GTCTTCCTTTCTTTGTAATACATCCTCATCTGTTCTGC 374

RESULT 5
US-09-925-065A-114513
; Sequence 114513, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114513
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-114513
```

Query Match 15.3%; Score 30.8; DB 6; Length 613;
Best Local Similarity 56.0%; Pred. No. 6.3;
Matches 56; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATCGCTTTTCCTATCAATAGTTTCTAA 96
DB 367 CATCCCTTAAACTTCCCTGGCGCTGATGTCCTTTGTCRGATCTGTGATTTATAGATCCCA 426

QY 97 CTCATGTCAGTCTTGCATCACAACCTCCCTTCAGTTGTAC 136
DB 427 GTCTTCTCTTCTTTGTAATACATCCTCATTCGTCTGTC 466

RESULT 6

US-09-925-065A-54797/c
; Sequence 54797, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54797
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-54797

Query Match 15.3%; Score 30.8; DB 6; Length 638;
Best Local Similarity 57.1%; Pred. No. 6.4;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 66 TATATCGTTTCCCTATCAATAGTTTCTAACTCATGTCAGTCTTGGATCAACCTCC 125
DB 627 TCTGTAGATATTACTCATGTCAGTGTGAGAAAATCATCCAGTCGATGCCAGCATTTCTCC 568

QY 126 TTCAGTTGTACCGCTACATCTGACAACTCCACAGTC 163
DB 567 TTCCCATGATCTGCTAGTTTGCAAAATATTCAGGTC 530

RESULT 7

US-09-925-065A-446887
; Sequence 446887, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 446887
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-446887

Query Match 15.1%; Score 30.4; DB 6; Length 583;
Best Local Similarity 63.9%; Pred. No. 8.3;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTCCTTATCGCTTTTCCTATCAATAGTTTCTAA 96
DB 135 CCTCATTAATCTTCCAAGAGAGCTTCCCTGTCTCGGTTTGGCATATCTCTCT 194

QY 97 CTCATGTCAGTC 108
DB 195 TTCATGTGGGTC 206

RESULT 8

US-09-925-065A-146565/c
; Sequence 146565, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146565
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-146565

Query Match 15.0%; Score 30.2; DB 6; Length 458;
Best Local Similarity 60.2%; Pred. No. 8.9;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAAGAGAGTAGCAAACTGTTTACACCCCGAGACAGTTCCTATATCGC 73
DB 214 TTGATGATGAAAAGTGAATGCTAACTGATTGCACACCGTCCCATACCTTACATAGA 155

QY 74 TTTTCCCTATCAATAGTTTCTAA 96
DB 154 TTATCTTATTATTGTTGCTAA 132

RESULT 9

US-09-925-065A-22533
; Sequence 22533, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single

```
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22533
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-22533

Query Match          15.0%; Score 30.2; DB 6; Length 520;
Best Local Similarity 58.2%; Pred. No. 9.3;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 CCCGACAGAGTGGCCCTATATCGCTTTTCCCTATCAATAGTTTCTAACTCATGTGTCAGTCT 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 CCGACACAGCGCCAGTGTTCCTATGCTCATCAATATTATTTCTTTGTTGCTGGAT 233

QY 110 TCGGATCACAACTCTTCAGTTGTACCGCT 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 GGTGCTTGTAAACTCTCAAGGTGTGCTCCT 264

RESULT 10
US-09-925-065A-22534
; Sequence 22534, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22534
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-22534

Query Match          15.0%; Score 30.2; DB 6; Length 520;
Best Local Similarity 58.2%; Pred. No. 9.3;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 CCCGACAGAGTGGCCCTATATCGCTTTTCCCTATCAATAGTTTCTAACTCATGTGTCAGTCT 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 CCGACACAGCGCCAGTGTTCCTATGCTCATCAATATTATTTCTTTGTTGCTGGAT 233

QY 110 TCGGATCACAACTCTTCAGTTGTACCGCT 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 GGTGCTTGTAAACTCTCAAGGTGTGCTCCT 264

RESULT 11
US-09-925-065A-700722/c
; Sequence 700722, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700722
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-700722

Query Match          15.0%; Score 30.2; DB 6; Length 2072;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAGAGAGTAGTACGAAACCTGTTACACCCCGGACAGACAGTTGCCCTATATCCG 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 951 TTGATGATGAAAGTGAATGCTAACTGATTGCACACCCAGGTGCCCATACCTTACATAGA 892

QY 74 TTTTCCCTATCAATAGTTTCTAA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 891 TTAUCTTATTAAATTGTTGCTTAA 869

RESULT 12
US-09-925-065A-700723/c
; Sequence 700723, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700723
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-700723
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Db 234 GGTGCTTGTAAACTCTCAAGGTGTGCTCCT 264

RESULT 11
US-09-925-065A-700722/c
; Sequence 700722, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700722
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-700722

Query Match          15.0%; Score 30.2; DB 6; Length 2072;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAGAGAGTAGTACGAAACCTGTTACACCCCGGACAGACAGTTGCCCTATATCCG 73
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Db 951 TTGATGATGAAAGTGAATGCTAACTGATTGCACACCCAGGTGCCCATACCTTACATAGA 892

QY 74 TTTTCCCTATCAATAGTTTCTAA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 891 TTAUCTTATTAAATTGTTGCTTAA 869

RESULT 12
US-09-925-065A-700723/c
; Sequence 700723, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 700723
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-700723
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OM nucleic - nucleic search, using sw model

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	102	50.7	2340	US-09-614-221A-299	Sequence 299, Appl
2	35.2	17.5	5622	US-09-067-800-3	Sequence 3, Appli
3	35.2	17.5	5622	US-09-349-677-3	Sequence 3, Appli
4	32	15.9	4953	US-09-620-312D-240	Sequence 240, App
5	31.6	15.7	1914	US-09-489-039A-2072	Sequence 2072, Ap
6	31.4	15.6	28932	US-09-949-016-16653	Sequence 16653, A
7	31	15.4	5583	US-09-312-283C-372	Sequence 372, App
8	30.8	15.3	1797	US-09-248-796A-5087	Sequence 5087, Ap
9	30.4	15.1	642	US-09-533-559-6096	Sequence 6096, Ap
10	30.2	15.0	128516	US-09-949-016-13501	Sequence 13501, A
11	30.2	15.0	133157	US-09-949-016-12541	Sequence 12541, A
12	30	14.9	69263	US-09-949-016-12594	Sequence 12594, A
13	30	14.9	69709	US-09-949-016-16036	Sequence 16036, A
14	29.8	14.8	390416	US-09-949-016-16923	Sequence 16923, A
15	29.6	14.7	832	US-09-621-976-2813	Sequence 2813, Ap
16	29.6	14.7	2508	US-09-949-016-1466	Sequence 1466, A
17	29.6	14.7	97989	US-09-949-016-13208	Sequence 13208, A
18	29.4	14.6	896	US-09-067-800-5	Sequence 5, Appli
19	29.4	14.6	896	US-09-349-677-5	Sequence 5, Appli
20	29.4	14.6	896	US-09-981-087A-3	Sequence 3, Appli
21	29.4	14.6	896	US-09-978-382A-3	Sequence 3, Appli
22	29.4	14.6	896	US-09-978-740A-3	Sequence 3, Appli
23	29.4	14.6	896	US-09-978-729A-3	Sequence 3, Appli
24	29.4	14.6	896	US-09-978-730-3	Sequence 3, Appli

C 25	29.4	14.6	1213	2	US-08-554-612C-14	Sequence 14, Appl
C 26	29.4	14.6	95318	3	US-09-949-016-11784	Sequence 11784, A
C 27	29.4	14.6	95318	3	US-08-949-016-13998	Sequence 13998, A
C 28	29.2	14.5	601	3	US-09-949-016-64625	Sequence 64625, A
C 29	29.2	14.5	36311	3	US-09-949-016-13627	Sequence 13627, A
C 30	29	14.4	319608	3	US-09-539-333D-1	Sequence 1, Appli
C 31	29	14.4	319608	3	US-09-679-409-1	Sequence 1, Appli
C 32	28.8	14.3	7813	3	US-09-573-080A-27	Sequence 27, Appli
C 33	28.6	14.2	1308	3	US-09-489-039A-116	Sequence 116, App
C 34	28.6	14.2	171700	3	US-09-949-016-12276	Sequence 12276, A
C 35	28.6	14.2	171701	3	US-09-949-016-15835	Sequence 15835, A
C 36	28.4	14.1	10718	3	US-09-949-016-11918	Sequence 11918, A
C 37	28.4	14.1	10718	3	US-09-949-016-13816	Sequence 13816, A
C 38	28.2	14.0	1521	2	US-08-670-354-3	Sequence 3, Appli
C 39	28.2	14.0	1521	3	US-09-320-424-3	Sequence 3, Appli
C 40	28.2	14.0	1521	3	US-09-825-563-3	Sequence 3, Appli
C 41	28.2	14.0	1521	6	PCT-US96-10895-3	Sequence 3, Appli
C 42	28.2	14.0	1606	3	US-09-919-039-117	Sequence 117, App
C 43	28.2	14.0	1711	3	US-09-569-611C-15	Sequence 15, Appli
C 44	28.2	14.0	1751	2	US-08-670-354-1	Sequence 1, Appli
C 45	28.2	14.0	1751	3	US-09-320-424-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-614-221A-299
; Sequence 299, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH STEROL SYNTHESIS AND METABOLISM
; FILE OF INVENTION: 16516.075
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 299
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-299

Query Match 50.7%; Score 102; DB 3; Length 2340;
Best Local Similarity 100.0%; Pred. No. 3.5e-25;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 100 ATGTGAGTCTTGGATCACAACCTCTTCAGTTGTACCGCTACATCTGCAACATCCACC 159
DB 1 ATGTGAGTCTTGGATCACAACCTCTTCAGTTGTACCGCTACATCTGCAACATCCACC 60
QY 160 AGTCGAAAACAGAACAGGACCATCGCTATTGCACTCTGCA 201
DB 61 AGTCGAAAACAGAACAGGACCATCGCTATTGCACTCTGCA 102

RESULT 2
US-09-067-800-3/c
; Sequence 3, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP

```
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5622
; OTHER INFORMATION: /label= AGL1_promoter
;
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGL1 promoter."
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; US-09-067-800-3
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; Query Match 17.5%; Score 35.2; DB 3; Length 5622;
; Best Local Similarity 58.7%; Pred. No. 0.077; 43; Indels 0; Gaps 0;
; Matches 61; Conservative 0; Mismatches 0;
;
; QY 66 TATATCGCTTTTCCCTATCAATAGTTTCTAACTCATGTCAGTCTTTCGCGATCACACCTCC 125
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; Db 2674 TATCTATTTTCCCTCTCCCTAGTTTCTTGCTACTCTCTGCGTGTGACTACTCCACC 2615
;
; QY 126 TTCAGTTGTACCGTACATCTGACACATCCACCATCCGACAGTCGCAAAA 169
; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 2614 TTCCTCCATTGATCATATATGACATCATCCAAATAATTAATAAA 2571
;
; RESULT 4
; US-09-620-312D-240/c
; Sequence 240, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 240
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Homo sapiens
;
;
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5622
; OTHER INFORMATION: /label= AGL1_promoter
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; OTHER INFORMATION: /note= "Nucleotide sequence of the AGL1 promoter."
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; US-09-067-800-3
;
; Query Match 17.5%; Score 35.2; DB 3; Length 5622;
; Best Local Similarity 58.7%; Pred. No. 0.077; 43; Indels 0; Gaps 0;
; Matches 61; Conservative 0; Mismatches 0;
;
; QY 66 TATATCGCTTTTCCCTATCAATAGTTTCTAACTCATGTCAGTCTTTCGCGATCACACCTCC 125
; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 2674 TATCTATTTTCCCTCTCCCTAGTTTCTTGCTACTCTCTGCGTGTGACTACTCCACC 2615
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; QY 126 TTCAGTTGTACCGTACATCTGACACATCCACCATCCGACAGTCGCAAAA 169
; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 2614 TTCCTCCATTGATCATATATGACATCATCCAAATAATTAATAAA 2571
;
; RESULT 3
; US-09-349-677-3/c
; Sequence 3, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4953)
US-09-620-312D-240

Query Match      15.9%; Score 32; DB 3; Length 4953;
Best Local Similarity 65.3%; Pred. No. 0.95;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 37 CCTGTTTACACCCCGAGAGAGTGCCTATATCGCTTTTCCCTATCAATAGTTCTTAA 96
Db 819 CCYCTTTAACTTCCAGAGAGCTTCCCTGTATCGGTTTGGCCCTTATCTCTCT 760
Qy 97 CTCATGTCAGTC 108
Db 759 TTCATTGGGTC 748

RESULT 5
US-09-489-039A-2072
; Sequence 2072, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2072
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1300), (1329)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-2072

Query Match      15.7%; Score 31.6; DB 3; Length 1914;
Best Local Similarity 60.5%; Pred. No. 0.92;
Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 18 TAGCAGAGAGTACGAACTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTT 77
Db 122 TAAACAGCGCGTGGCGGAAACGGTATAAATCGAGCGGAAAAAACCACGATATAGCGTTT 181
Qy 78 CCTATCAATAGTTTCTAATCATGT 103
Db 182 CGCGTGCATTAATTTATACATATT 207

RESULT 6
US-09-949-016-16653/C
; Sequence 16653, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16653
; LENGTH: 28932
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16653

Query Match      15.6%; Score 31.4; DB 3; Length 28932;
Best Local Similarity 50.3%; Pred. No. 3;
Matches 77; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 24 AGAGAGTACGAACCTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTTCCCTAT 83
Db 27038 AAAAAGTGCTAAACATATTTACAGCAATGTGCTAAGTCTGAGTTAAATTCAGAT 26979
Qy 84 CAATAGTTTCTTAATCTATGTCAGTCTTGGATCACACCTCTTACGCTTACCGCTACA 143
Db 26978 CTAGACAAAAAATCTGAGGCTAAGCTTTATGTCAACAAGTTTACAAGTCCCTCCACA 26919
Qy 144 TCTGACAAACATCCACCAGTCGCAAAACAGAA 176
Db 26918 TATCAATACATAGGCATTACAGAACCAACA 26886

RESULT 7
US-09-312-283C-372
; Sequence 372, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 5583
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-372

Query Match      15.4%; Score 31; DB 3; Length 5583;
Best Local Similarity 50.3%; Pred. No. 2.2;
Matches 76; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 24 AGAGAGTACGAACCTGTTTACACCCCGAGAGAGTGGCCCTATATCGCTTTTCCCTAT 83
Db 601 AGAGCGGAGGAAAGACGTGTCTTCTGTCTCTCTCTGCTCTCTGCTCTCTCTGCTCTCT 660
Qy 84 CAATAGTTTCTTAATCTATGTCAGTCTTGGATCACACCTCTTACGCTTACCGCTACA 143
Db 661 TACTGTGTGAGCATCTCTCGGGGTGCTGTGGGTGCAAGACGCGGCAAGAACTGGGCC 720
Qy 144 TCTGACAAACATCCACCAGTCGCAAAACAGAA 174
Db 721 TCGGACACCGTCCACTTTTACGCAACCGAA 751

RESULT 8
US-09-248-796A-5087
; Sequence 5087, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5087
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5087

Query Match          15.3%; Score 30.8; DB 3; Length 1797;
Best Local Similarity 58.9%; Pred. No. 1.7;
Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 68 TATCGCTTTCCCTATCAATAGTTTCTAACTCATGTGTCAGTCTTGGCATCACAACTCCTT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1556 TATCACTTTTACCTGGATTCAAAAATAGAAATAATGTGTCAGATTTTAGATCATTCCTCCAG 1615

QY 128 CAGTTCTACCGCTACATCTGACAAATCCA 157
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1616 AGGAGTGCCATTACATGTGAGAACGCCA 1645

RESULT 9
US-09-533-559-6096
; Sequence 6096 Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6096
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(642)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-6096

Query Match          15.1%; Score 30.4; DB 3; Length 642;
Best Local Similarity 59.1%; Pred. No. 1.6;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 110 TCGATACCAACTCCTTTCAGTTGTACCGTACATCTGACAAATCCACACGTCGCAAAA 169
Db 261 TGAATCGCGCTCCCGTCAGTCTTGCAGCGTACATCCGTCAACGTCACACGTCGACAT 320

QY 170 CAGACAGGAACCATCGCTATTGCATC 197
Db 321 CTGGGATGAAGCCCGCACCAACCGCCAC 348

RESULT 10
US-09-949-016-13501
; Sequence 13501 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12541
; LENGTH: 133157
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13501

Query Match          15.0%; Score 30.2; DB 3; Length 133157;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAACAGAGTAGCAAAACCTGTTTACACCCCGGACAGACAGTTGCCCTATATCGC 73
Db 35612 TTGATGATGAAAAGTGAATGCTAACTGATTGCACACACGTCGCCCATACCTTACATAGA 35685

QY 74 TTTTCCTATCAATAGTTTCTAA 96
Db 35686 TTATCTTATTTAATTGTTGCTAA 35708

RESULT 11
US-09-949-016-12541
; Sequence 12541 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12541
; LENGTH: 133157
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12541

Query Match          15.0%; Score 30.2; DB 3; Length 133157;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 14 TTCATAAGCAACAGAGTAGCAAAACCTGTTTACACCCCGGACAGACAGTTGCCCTATATCGC 73
Db 35612 TTGATGATGAAAAGTGAATGCTAACTGATTGCACACACGTCGCCCATACCTTACATAGA 35671

QY 74 TTTTCCTATCAATAGTTTCTAA 96
Db 35672 TTATCTTATTTAATTGTTGCTAA 35694
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RESULT 12
US-09-949-016-12594
; Sequence 12594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12594
; LENGTH: 69263
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(69263)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12594

Query Match 14.9%; Score 30; DB 3; Length 69263;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 59 GTTGGCCCTATATCGCTTTCCCTATCAATGTTTCTTAACATCAATGTCAGTCTTGGATCAC 118
DB 53870 GTCTCACTATGTGGTTTGGCCGCTCTCTAAGTCTTCAAGTGTATCTCTGCTC 53929

QY 119 AACTCTCTTCACTGTTGACCGCTACATCTGACAAACATCCACAGTCGCAAA 168
DB 53930 AGCTTCCCAAAGTTGTGGGATTACAGGTGTGAACACTACCACCTGTCCCCAA 53979

Query Match 14.9%; Score 30; DB 3; Length 69263;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 59 GTTGGCCCTATATCGCTTTCCCTATCAATGTTTCTTAACATCAATGTCAGTCTTGGATCAC 118
DB 53870 GTCTCACTATGTGGTTTGGCCGCTCTCTAAGTCTTCAAGTGTATCTCTGCTC 53929

QY 119 AACTCTCTTCACTGTTGACCGCTACATCTGACAAACATCCACAGTCGCAAA 168
DB 53930 AGCTTCCCAAAGTTGTGGGATTACAGGTGTGAACACTACCACCTGTCCCCAA 53979

RESULT 13
US-09-949-016-16036
; Sequence 16036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16036
; LENGTH: 69709
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(69709)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16036

Query Match 14.9%; Score 30; DB 3; Length 69709;
Best Local Similarity 54.5%; Pred. No. 13;

Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 59 GTTGGCCCTATATCGCTTTCCCTATCAATGTTTCTTAACATCAATGTCAGTCTTGGATCAC 118
DB 53870 GTCTCACTATGTGGTTTGGCCGCTCTCTAAGTCTTCAAGTGTATCTCTGCTC 53929

QY 119 AACTCTCTTCACTGTTGACCGCTACATCTGACAAACATCCACAGTCGCAAA 168
DB 53930 AGCTTCCCAAAGTTGTGGGATTACAGGTGTGAACACTACCACCTGTCCCCAA 53979

RESULT 14
US-09-949-016-16923
; Sequence 16923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16923
; LENGTH: 390416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16923

Query Match 14.8%; Score 29.8; DB 3; Length 390416;
Best Local Similarity 54.0%; Pred. No. 29;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 86 ATAGTTTCTAATCACTGTCAGTCTTGGATCACAACTCTTTCAGTTGTACCGTACATC 145
DB 194856 ATAGTTTAGCTCTCAGGGAACAATTTTATTTTCTTAACTTCTTGGGAGACACC 194915

QY 146 TGACAAATCCACAGTCGCAAAACAGACAGGAAACATCGCTTATTCACCTCT 198
DB 194916 TTATGTATCCAAAGACTAACACACCATCAGAGTGCAAAATTCACCTCT 194968

RESULT 15
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 14.7%; Score 29.6; DB 3; Length 832;

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:36:26 ; Search time 173.375 Seconds
(without alignments)
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Title: US-10-041-018-399_COPY_10000_10200

Perfect score: 201

Sequence: 1 aagaagtagcacattcataa.....catcgctattgcactctgca 201

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA_Main:*
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10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	201	100.0	39827	7	US-10-041-018-399
2	102	50.7	2340	8	US-10-793-639-299
3	35.2	17.5	5622	9	US-10-871-651A-5
4	32	15.9	657	3	US-09-864-761-20243
5	32	15.9	1216	9	US-10-450-763-7959
6	32	15.9	1367	9	US-10-450-763-27115
7	32	15.9	1857	9	US-10-450-763-8929
8	32	15.9	1976	3	US-09-864-761-3473
9	32	15.9	2365	9	US-10-450-763-8921
10	32	15.9	3118	9	US-10-450-763-6475
11	32	15.9	4953	5	US-10-037-270-240
12	32	15.9	4953	6	US-10-117-722-240
13	32	15.9	4953	9	US-10-450-763-6466
14	32	15.9	4953	9	US-10-450-763-27114
15	32	15.9	4953	9	US-10-122-851-240
16	32	15.9	5861	3	US-09-814-353-21084
17	32	15.9	87731	5	US-10-087-192-1342
18	31.6	15.7	3683	8	US-10-473-126-194
19	31.2	15.5	581	4	US-09-925-065A-194717
20	31.2	15.5	613	4	US-09-925-065A-114512
21	31.2	15.5	21537	6	US-10-311-455-1972
22	31	15.4	661	6	US-10-029-386-22736
23	31	15.4	3345	5	US-10-027-632-112866

C	24	31	15.4	3345	6	US-10-027-632-112866	Sequence 112866,
	25	31	15.4	5583	3	US-09-866-050A-372	Sequence 372, App
	26	31	15.4	5583	5	US-10-152-661-372	Sequence 372, App
	27	30.8	15.3	581	4	US-09-925-065A-114514	Sequence 114514,
	28	30.8	15.3	613	4	US-09-925-065A-114513	Sequence 114513,
C	29	30.8	15.3	638	4	US-09-925-065A-54797	Sequence 54797, A
C	30	30.8	15.3	1168	3	US-09-764-875-260	Sequence 260, App
	31	30.8	15.3	1271	3	US-09-764-853-212	Sequence 212, App
	32	30.8	15.3	2038	3	US-09-887-280-2	Sequence 2, Appli
	33	30.8	15.3	2230	3	US-09-887-280-1	Sequence 1, Appli
	34	30.6	15.2	600	9	US-10-972-079-56170	Sequence 56170, A
	35	30.6	15.2	856	7	US-10-425-114-8228	Sequence 8228, Ap
C	36	30.4	15.1	500	9	US-10-450-763-3573	Sequence 3573, Ap
	37	30.4	15.1	503	3	US-09-867-701-10117	Sequence 10117, A
	38	30.4	15.1	583	4	US-09-925-065A-446887	Sequence 446887,
	39	30.4	15.1	642	8	US-10-653-047-6086	Sequence 6086, Ap
C	40	30.4	15.1	1548	9	US-10-450-763-7965	Sequence 7965, Ap
C	41	30.4	15.1	1761	9	US-10-450-763-3581	Sequence 3581, Ap
C	42	30.4	15.1	1761	9	US-10-450-763-6469	Sequence 6469, Ap
C	43	30.4	15.1	1761	9	US-10-450-763-7961	Sequence 7961, Ap
C	44	30.4	15.1	2082	9	US-10-450-763-8931	Sequence 8931, Ap
	45	30.4	15.1	2445	5	US-10-027-632-110856	Sequence 110856,

ALIGNMENTS

RESULT 1

US-10-041-018-399
; Sequence 399, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080051/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 399
; LENGTH: 39827
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-041-018-399

Query Match	100.0%;	Score 201;	DB 7;	Length 39827;
Best Local Similarity	100.0%;	Pred. No. 1.6e-57;		
Matches 201;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGAAGTAGCACATTCAATAGCAAGAGAGTAGCAAAACCTGTTTACACCCCGGAGACAGT	60	
Db	10000	AAGAAGTAGCACATTCAATAGCAAGAGAGTAGCAAAACCTGTTTACACCCCGGAGACAGT	10059	
QY	61	TGCCCTATATCGCTTTTCCCTATCAATGTTTCTACTCATGTCAGTCTTGGCATCAAA	120	
Db	10060	TGCCCTATATCGCTTTTCCCTATCAATGTTTCTACTCATGTCAGTCTTGGCATCAAA	10119	
QY	121	CTTCCTTCAGTTTGTACCGGTACATCTGCAAAACATCCACAGTCGCAAAACAGAACAGGAA	180	
Db	10120	CTTCCTTCAGTTTGTACCGGTACATCTGCAAAACATCCACAGTCGCAAAACAGAACAGGAA	10179	
QY	181	CCATCGCTATTGCACCTTGCA	201	
Db	10180	CCATCGCTATTGCACCTTGCA	10200	

RESULT 2

US-10-793-639-299
; Sequence 299, Application US/10793639
; Publication No. US20040199940A1

Qy	Db	126	TTTCAGTTGTACCGCTACATCTGACAAATCCACCATCCAGTTCGCAAAA	169
		2614	TTCTCCATTGATCCATATATGACATCACCATAATTAATAA	2571
<p>GENERAL INFORMATION:</p> <p>APPLICANT: Karunandaa, Balasulojini</p> <p>APPLICANT: Yu, Jaehyuk</p> <p>APPLICANT: Kishore, Ganesh M.</p> <p>TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH STEROL SYNTHESIS AND METABOLISM</p> <p>TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM</p> <p>FILE REFERENCE: 16516.075</p> <p>CURRENT APPLICATION NUMBER: US/10/793,639</p> <p>PRIOR FILING DATE: 2004-03-05</p> <p>PRIOR APPLICATION NUMBER: US/09/614,221A</p> <p>PRIOR FILING DATE: 2000-07-11</p> <p>PRIOR APPLICATION NUMBER: US 60/142,981</p> <p>PRIOR FILING DATE: 1999-07-12</p> <p>NUMBER OF SEQ ID NOS: 626</p> <p>SEQ ID NO 299</p> <p>TYPE: DNA</p> <p>ORGANISM: Saccharomyces cerevisiae</p> <p>US-10-793-639-299</p>				
<p>Query Match 50.7%; Score 102; DB 8; Length 2340;</p> <p>Best Local Similarity 100.0%; Pred. No. 4.9e-24;</p> <p>Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>				
Qy		100	ATGTCAGTCTTCGGATCAACAACCTCTTCAGTTGTACCGCTACATCTGACAAATCCACC	159
Db		1	ATGTCAGTCTTCGGATCAACAACCTCTTCAGTTGTACCGCTACATCTGACAAATCCACC	60
Qy		160	AGTCGCAAAACAGACAGAACCTCGCTATTGCACTGCA	201
Db		61	AGTCGCAAAACAGACAGAACCTCGCTATTGCACTGCA	102
<p>RESULT 3</p> <p>US-10-871-651A-5/c</p> <p>Sequence 5, Application US/10871651A</p> <p>Publication No. US20050120417A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Yanofsky, Martin F.</p> <p>APPLICANT: Liljgren, Sarah</p> <p>APPLICANT: The Regents of the University of California</p> <p>TITLE OF INVENTION: Control of Fruit Dehiscence in Arabidopsis by</p> <p>TITLE OF INVENTION: Indehiscent1 Genes</p> <p>FILE REFERENCE: 19452A-000710US</p> <p>CURRENT APPLICATION NUMBER: US/10/871,651A</p> <p>CURRENT FILING DATE: 2004-06-18</p> <p>PRIOR APPLICATION NUMBER: US 60/090,649</p> <p>PRIOR FILING DATE: 1998-06-25</p> <p>PRIOR APPLICATION NUMBER: US 09/339,998</p> <p>PRIOR FILING DATE: 1999-06-25</p> <p>PRIOR APPLICATION NUMBER: US 09/548,971</p> <p>PRIOR FILING DATE: 2000-04-13</p> <p>NUMBER OF SEQ ID NOS: 28</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 5</p> <p>LENGTH: 5622</p> <p>TYPE: DNA</p> <p>ORGANISM: Arabidopsis sp.</p> <p>FEATURE:</p> <p>OTHER INFORMATION: SHATTERPROOF1 (SHP1) genomic sequence</p> <p>FEATURE:</p> <p>NAME/KEY: modified base</p> <p>LOCATION: (935)...(941)</p> <p>OTHER INFORMATION: n = g, a, c or t</p> <p>US-10-871-651A-5</p>				
<p>Query Match 17.5%; Score 35.2; DB 9; Length 5622;</p> <p>Best Local Similarity 58.7%; Pred. No. 0.58;</p> <p>Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;</p>				
Qy		66	TATATCGCTTTCCCTATCAATAGTTTCTPAATCAATGTCAGTCTTCGATCACAACCTCC	125
Db		2674	TATCTTATTTTCCCTCTCCCTAGTTTCTTGTCTCTCTGCTGCTGCTACTCCACC	2615

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; OTHER INFORMATION: NT HIT: M10976.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P10262, EVALUE 3.00e-30
US-09-864-761-20243

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Query Match 15.9%; Score 32; DB 3; Length 657;
Best Local Similarity 65.3%; Pred. No. 3.1;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

[illegible]

Qy 97 CTCATGTCAGTC 108
|||||
Db 527 TTCATTGGGTC 538

RESULT 5
US - 10-450-763-7959/c
; Sequence 7959, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

```

; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Cusdom
; SEQ ID NO 7959
; LENGTH: 1216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (151)..(1143)
; OTHER INFORMATION: 39% homologous to Fowlpox virus gag, accession number
; OTHER INFORMATION: AF006065, Smith-Waterman Score=556.
US-10-450-763-7959

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Query Match 15.9%; Score 32; DB 9; Length 1216;
Best Local Similarity 65.3%; Pred. No. 4;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

[illegible]

Qy 97 CTCATGTCAGTC 108
|||||
Db 609 TTCATTGGGTC 598

RESULT 6
US-10-450-763-27115
; Sequence 27115, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hvsseg, Inc

```

FILE OF INVENTION: NOVEL NUCLEIC ACIDS
FILE REFERENCE: 790CI3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-05-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31

```

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; PRIOR APPLICATION NUMBER: 09/649,167
;
; PRIOR FILING DATE: 2000-08-23
;
; NUMBER OF SEQ ID NOS: 60736
;
; SOFTWARE: Custom
;
; SEQ ID NO 27115
;
; LENGTH: 1367
;

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1066)..(74)
; OTHER INFORMATION: 39%
; OTHER INFORMATION: AF0
US-10-450-763-27115

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Query Match 15.9%; Score 32; DB 9; Length 1367;
Best Local Similarity 65.3%; Pred. No. 4.1;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

[illegible]

Qy 97 CTATGTCAGTC 108
Db 608 TTCAATTTGGGTC 619

RESULT 7
US-10-450-763-8929/c
; Sequence 8929, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

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; FILE REFERENCE: 790CI23/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 8929
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (800)..(1792)
; OTHER INFORMATION: 33% homologous to F01
; OTHER INFORMATION: AF006065, Smith-Waterm
; US-10-450-763-8929

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Query Match 15.9%; Score 32; DB 9; Length 1857;
Best Local Similarity 65.3%; Pred. No. 4.7;
Matches 47: Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGAGAGAGTGCCTTATATCGCTTTTCCCTATCAATAGTTTCTAA 96

Dh 1318 CCTCTTTATATCGCTTCCATAGAGAGGCTTCCCTATATCGGTTTATGCGCTTTCATATCCCTCT 1259

QY 97 CTCAATGTCAGTC 108
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1258 TTTCAATTTCCCTC 1241

RESULT 8
US-09-864-761-3473
; Sequence 3473, Application US/09864761

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/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharron G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aemica-X-1
/ CURRENT APPLICATION NUMBER: US 09/864,761
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 3473
/ LENGTH: 1976
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AL023280.1
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
/ OTHER INFORMATION: EXPRESSED IN HL100, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
/ US-09-864-761-3473
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Query Match 15.9%; Score 32; DB 3; Length 1976;
Best Local Similarity 65.3%; Pred. No. 4.8;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 37 CCTGTTTACACCCCGAGACAGCTTCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 895 CCTCTTTATCCTTCCAGAGAGCTTCCCTGTATCGTTAGCCTTTGATATCCTCTCT 954
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QY 97 CTCATGTGAGTC 108
Db 955 TTCATTGGGTC 966

RESULT 9
US-10-450-763-8921/c
/ Sequence 8921, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 8921
/ LENGTH: 2365
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (74)..(2362)
/ OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
/ OTHER INFORMATION: polyprotein gpr80, accession number M18247, Smith-Waterman Score=
US-10-450-763-8921
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Query Match 15.9%; Score 32; DB 9; Length 2365;
Best Local Similarity 65.3%; Pred. No. 5.1;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 37 CCTGTTTACACCCCGAGACAGCTTCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 586 CCTCTTTATCCTTCCAGAGAGCTTCCCTGTATCGTTAGCCTTTGATATCCTCTCT 527
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QY 97 CTCATGTGAGTC 108
Db 526 TTCATTGGGTC 515
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RESULT 10
US-10-450-763-6475/c
/ Sequence 6475, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 6475
/ LENGTH: 3118
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (66)..(2366)
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OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
OTHER INFORMATION: polyprotein gPr80, accession number AF052723, Smith-Waterman Score=1547.
US-10-450-763-6475

Query Match 15.9%; Score 32; DB 9; Length 3118;
Best Local Similarity 65.3%; Pred. No. 5.7;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTTCCTATCAATAGTTTCTAA 96
DB 578 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGGTTTAGCGCTTGGCATATCCTCTCT 519
QY 97 CTCATGTCAGTC 108
DB 518 TTCATTGGGTC 507

RESULT 11
US-10-037-270-240/c
Sequence 240, Application US/10037270
Publication No. US20030104529A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyang
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Dmanac, Radoje T.

TITLE OF INVENTION: NO. US20030104529A1el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 240
LENGTH: 4953
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4953)
US-10-037-270-240

Query Match 15.9%; Score 32; DB 5; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTTCCTATCAATAGTTTCTAA 96
DB 819 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGGTTTAGCGCTTGGCATATCCTCTCT 760
QY 97 CTCATGTCAGTC 108
DB 759 TTCATTGGGTC 748

RESULT 12
US-10-117-722-240/c
Sequence 240, Application US/10117722
Publication No. US20030219744A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Dmanac, Radoje T.

TITLE OF INVENTION: NO. US20030219744A1el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 240
LENGTH: 4953
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4953)
US-10-117-722-240

Query Match 15.9%; Score 32; DB 6; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTTCCTATCAATAGTTTCTAA 96
DB 819 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGGTTTAGCGCTTGGCATATCCTCTCT 760
QY 97 CTCATGTCAGTC 108
DB 759 TTCATTGGGTC 748

RESULT 13
US-10-450-763-6466/c
Sequence 6466, Application US/10450763
Publication No. US20050196754A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 6466
LENGTH: 4953
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (308)..(2608)
OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
OTHER INFORMATION: polyprotein gPr80, accession number AF052723, Smith-Waterman Score=1547.

US-10-450-763-6466

Query Match 15.9%; Score 32; DB 9; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 820 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGGTTTAGCCTTTGCATATCCTCTCT 761
QY 97 CTCATGTCAGTC 108
Db 760 TTCATTGGGTC 749

RESULT 14

US-10-450-763-27114/c
; Sequence 27114, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450, 763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540, 217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649, 167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 27114
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (308)..(2608)
; OTHER INFORMATION: 43% homologous to Feline leukemia virus gag-pol precursor
; OTHER INFORMATION: polyprotein gPr80, accession number AF052723, Smith-Waterman Score=
; OTHER INFORMATION: 1547.
US-10-450-763-27114

Query Match 15.9%; Score 32; DB 9; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 820 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGGTTTAGCCTTTGCATATCCTCTCT 761
QY 97 CTCATGTCAGTC 108
Db 760 TTCATTGGGTC 749

RESULT 15

US-10-122-851-240/c
; Sequence 240, Application US/10122851
; Publication No. US20050239060A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BDV3
; CURRENT APPLICATION NUMBER: US/10/122, 851
; CURRENT FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 240
; LENGTH: 4953
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4953)
US-10-122-851-240
Query Match 15.9%; Score 32; DB 9; Length 4953;
Best Local Similarity 65.3%; Pred. No. 6.9;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 37 CCTGTTTACACCCCGAGACAGTTGCCCTATATCGCTTTCCCTATCAATAGTTTCTAA 96
Db 819 CCTCTTTAATCCTTCCAAGAGAGCTTCCCTGTATCGGTTTAGCCTTTGCATATCCTCTCT 760
QY 97 CTCATGTCAGTC 108
Db 759 TTCATTGGGTC 748
Search completed: February 16, 2006, 07:57:37
Job time : 174.375 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 08:16:57 ; Search time 582.92 Seconds
(without alignments)
2854.981 Million cell updates/sec

Title: US-10-041-018-383

Perfect score: 4113

Sequence: 1 MNLSLCTASPLTKSRPAA.....TVKDIINPLVLVNEEQR 784

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abseq04
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-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:

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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144	3.5	7512	8 US-10-647-956A-7	Sequence 7, Appli
2	137	3.3	3919	12 US-11-108-172-1125	Sequence 1125, Ap
3	133.5	3.2	8503	12 US-11-124-368A-45	Sequence 45, Appl
4	133.5	3.2	8512	12 US-11-124-368A-46	Sequence 46, Appl

5	131.5	3.2	3444	8	US-10-793-626-4144	Sequence 4144, Ap
6	125	3.0	3735	12	US-11-052-554A-514	Sequence 514, App
7	123.5	3.0	15475	7	US-10-893-483-4	Sequence 4, Appli
8	122.5	3.0	1331	8	US-10-485-517-111	Sequence 111, App
9	121.5	3.0	3729	8	US-10-793-626-3667	Sequence 3667, Ap
10	121.5	3.0	6773	8	US-10-947-249-105	Sequence 105, App
11	121.5	3.0	15071	8	US-10-793-626-2963	Sequence 2963, Ap
12	121	2.9	3146	8	US-10-793-626-3375	Sequence 3375, Ap
13	121	2.9	3569	8	US-10-793-626-4304	Sequence 4304, Ap
14	120.5	2.9	3684	8	US-10-793-626-95	Sequence 95, Appli
15	120.5	2.9	3906	8	US-10-793-626-3870	Sequence 3870, Ap
16	119.5	2.9	2970	8	US-10-793-626-2593	Sequence 2593, Ap
17	119.5	2.9	3549	8	US-10-793-626-3796	Sequence 3796, Ap
18	119.5	2.9	3815	8	US-10-750-185-29584	Sequence 29584, A
19	119.5	2.9	3815	8	US-10-750-623-29584	Sequence 29584, A
20	119.5	2.9	5264	7	US-10-766-317-7	Sequence 7, Appli
21	119.5	2.9	5575	12	US-11-136-527-3245	Sequence 3245, Ap
22	119.5	2.9	14121	12	US-11-124-020A-1	Sequence 10, Appl
23	119.5	2.9	14121	12	US-11-123-656A-3	Sequence 3, Appli
24	118.5	2.9	10170	12	US-11-136-527-1817	Sequence 1817, Ap
25	117	2.8	29942	7	US-10-895-064-3	Sequence 3, Appli
26	117	2.8	29942	7	US-10-895-064-34	Sequence 34, Appl
27	117	2.8	29942	7	US-10-895-064-457	Sequence 457, App
28	117	2.8	29942	7	US-10-895-064-724	Sequence 724, App
29	117	2.8	29942	7	US-10-895-064-1319	Sequence 1319, Ap
30	117	2.8	29942	7	US-10-895-064-1908	Sequence 1908, Ap
31	117	2.8	29942	7	US-10-895-064-2454	Sequence 2454, Ap
32	116.5	2.8	1556	9	US-11-072-512-779	Sequence 779, App
33	116.5	2.8	43445	12	US-11-124-020A-1	Sequence 1, Appli
34	116.5	2.8	43445	12	US-11-124-020A-2	Sequence 2, Appli
35	116	2.8	3866	8	US-10-793-626-3980	Sequence 3980, Ap
36	115.5	2.8	3145	12	US-11-188-743-9	Sequence 9, Appli
37	115.5	2.8	3145	12	US-11-183-294-21	Sequence 21, Appl
38	115.5	2.8	5054	8	US-10-821-234-123	Sequence 123, App
39	115	2.8	4045	8	US-10-793-626-3929	Sequence 3929, Ap
40	115	2.8	4501	12	US-11-136-527-2885	Sequence 2885, Ap
41	114.5	2.8	2292	12	US-11-136-527-2676	Sequence 2676, Ap
42	114.5	2.8	3026	12	US-11-136-527-2868	Sequence 2868, Ap
43	114.5	2.8	3204	8	US-10-793-626-3940	Sequence 3940, Ap
44	114	2.8	3060	8	US-10-793-626-3495	Sequence 3495, Ap
45	114	2.8	10302	12	US-11-127-832-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-647-956A-7
; Sequence 7, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647,956A
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 7512
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
US-10-647-956A-7
Alignment Scores: 0.00197
Pred. No.: 144.00
Length: 7512
Matches: 149

Percent Similarity:	33.0%	Conservative:	118
Best Local Similarity:	18.4%	Mismatches:	257
Query Match:	3.5%	Indels:	284
DB:	8	Gaps:	40
US-10-041-018-383 (1-784) x US-10-647-956A-7 (1-7512)			
QY	36	AsnProThrAsnLeuIleleAspThrLysGluArgIleGlnLysGlnPheLysAsn	55
DB	7	AACTATTATCAAGCACTATCGATACTATTGTGCAGAAATGCAATTAATCTGTCOG---	63
QY	56	ValGluIleSerValSerSerTyraAspThrAlaTrpValAlaMetValProSerProAsn	75
DB	64	GCGGAATTCCTTTGATATCCCTTTGATCT-----	93
QY	76	SerProLysSerProCysPheProGluCysLeuAsnTrpLeuIleAsnGlnLeuAsn	95
DB	94	-----TTCCGGGAAAAACTCGGGGAATGGTTAAT-----	123
QY	96	AspGlySerTrpGlyLeuValAsnHisThrHisAsn-----	107
DB	124	-----TGGGGGAAGCAAAACGGATTATGAAATTCGCAAGCGGAACAGGATAGA	174
QY	108	-----HisAsnHisProLeuLeuLysAspSerLeu	117
DB	175	AACCTACTTCAGAAACGTATTTTGGCTATGCTAATCCGCTGCTGAAACCGCTGT	234
QY	118	SerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIle	137
DB	235	-----CGGTGGGTACCCGGCAAAATG	255
QY	138	AsnLysGlyLeuSerPheIleGlu-----SerAsnLeu-----	148
DB	256	-----TTGGGTTTATACAAGGTATAGTGATCTGTTGGTAATCGTGTGATAAC	306
QY	149	-----AlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAspIlePhe	166
DB	307	TATGCCCGCCGGGCTCGGTGATCGATGTTCTCACCGGGCGCTTAT-----	357
QY	167	ProGlyLeuLeuGluTyraLysAsnLeu-----AspIleAsnLeuLeuSer	182
DB	358	ACGGAATTCACCGTAGCAAGCAAAACTTGCATGACAGCAGCTCAATTTATACCTAGAT	417
QY	183	LysGlnThrAsp-----PheSerLeuMetLeuHisLysArgGluLeuGlnLys---	199
DB	418	AAACGTCCCGCGGATTTAGCAAGCTTAATGCTCAGCCAGAAAATATGATGAGGAAAT	477
QY	200	-----ArgCysHisSerAsnGluMetAspGlyTyraLeuAlaTyraIleSerGluGlyLeu	217
DB	478	TCACCGCTGGCTCTCTTAATGAATG-----TGCCCTTGGCGGGATCGAAACAAACAA	531
QY	218	GlyAsnLeuTyraAsp-----TrpAsnMetValLysLysTyraGlnMetLysAsnGlySer	235
DB	532	GGAAATCAAGATGAAGTGGATATGTTGTCAACTATTCGTTTAAGTGGAGAGACA	591
QY	236	ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys	255
DB	592	CCTTATCATCAGCTTATGAAACTGTTCTGTAATCGTTTCATGAACGTGATCCAGGA---	648
QY	256	LeuAsnTyraAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyraPro	275
DB	649	TTTGTGCTATTGTGCAG-----GCACCCATTGTT-----	678
QY	276	HisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis	295
DB	679	-----GCTGCTAAGCTCGATCTGCTGACITTTGTTGGTATTAGCTCC	720
QY	296	HisPheArgValGluIleLysAsnValLeuAspGluThrTyraArgCysTrpValGluArg	315
DB	721	CATATTTCGCAAGACTGATATAACTTGCTGATTGAGGATC-----CCGGAAAAA	771
QY	316	AspGluGlnIle-----PheMetAspValValThrCysAla	327
DB	1489	GAGACGCGCTATT-----TTGGCTAATTAATATCTCTCAGCAAGCT	1533
DB	772	GATGAAGCGCGCTTGATACGCTTTTATAAAACAACTTTGGCGATATTACTACTGCTCAG	831
QY	328	LeuAlaPheArgLeuLeuArgIleAsnGlyTyraGluValSerProAspProLeuAlaGlu	347
DB	832	TTAATGTCCCAAGTTATCTGCGCGGTATTATGCGCTCTCACCGAAGATATTGCTTAC	891
QY	348	IleThrAsnGluLeuAlaLeuLysAspGluTyraAlaLeuGluThrTyraHisAlaSer	367
DB	892	GTGACGACTTCATTA-----	909
QY	368	HisIleLeuTyraGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAspPhe	387
DB	910	CATGTTGGATATAGCAGTGATATT-----CTGGTTATCCGTTGGTGGTGGT	957
QY	388	LeuLysGluIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluVal	407
DB	958	GTGGGTAAAGTC-----GAAGTA	975
QY	408	GluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsn	427
DB	976	GTTCTGTTTACCCGAACACCATCGGATATTATACAGTCAGACCAAT-----TAT	1026
QY	428	IleGlnLeuTyra-----AsnValAspAsnThrArgIleLeuLysThrThrTyraHisSer	445
DB	1027	ATTGAGCTGATCCACAGGTCGCCACAAATTATTTGATC-----AAA	1068
QY	446	SerAsnIleSerAsnThrAspTyraLeuArgLeuAlaValGluAspPheTyraThrCysGln	465
DB	1069	TACAATCTTAAGCAATAGT-----TTTGGTTTGGATGATTTTATCTCTG-----	1110
QY	466	SerIleTyraArgGluGluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAsp	485
DB	1110	-----	1110
QY	486	GlnLeuLysPheAlaArgGlnLysThrAlaTyraCysTyraPheSerValAlaAlaThrLeu	505
DB	1110	-----	1110
QY	506	SerSerProGluLeuSerAspAlaArgIleSerTrp-----AlaLysAsnGlyIle	522
DB	1111	-----CAATAATAAAGATGTTCCGCTGATGCTGAGACTGAGATTGCCATAATCCCTAT	1161
QY	523	LeuThrThrValValAspAspPhePheAspIleGlyGlyThrIle-----AspGluLeu	540
DB	1162	CCTGATATGCTCAATAATCAAAAGTATGAATCACAGGCGACAATCAACGTAGTACTCT	1221
QY	541	ThrAsnLeuIleGlnCys---ValGluLysTrp-----	550
DB	1222	GACATATATCTCAGTATAGGTTTACAAGATGCGCATAGCGGTAGTTATATAATTTTGC	1281
QY	551	---AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAla	569
DB	1282	GCCAAATTTAAATAATGACCAA-----TACTCCCGGAAAGCTTTCCTGCTTAAA	1329
QY	570	LeuLysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspVal	589
DB	1330	ATGAATAAGCTTATCGGTTGCTC-----AAAGTACCAGCCCTC	1368
QY	590	ThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIle	609
DB	1369	TCCTTTGCTACGTTGGAGCGTATTGTTGATAGTGTTAATAGC-----	1410
QY	610	TrpThrArgAspAlaTyraValProThrLeuAsnGluTyraMetGluAsnAlaTyraValSer	629
DB	1411	---ACCAATCCATCAGCTTGGAGTATTAAACAAG-----	1443
QY	630	PheAlaLeuGlyProIleValLysProAlaIleTyraPheValGlyProLysLeuSerGlu	649
DB	1444	-----GTTATCGGGTAAATTTCTATTTATGATCGTTATGGCATCAGTAA	1488
QY	650	GluIleValGluSerSerGluTyraHisAsnLeuPheLysLeuMetSerThrGlnGlyArg	669
DB	1489	GAGACGCGCTATT-----TTGGCTAATTAATATCTCTCAGCAAGCT	1533

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Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 1534 GTTGGCAATCAGCTTAGCCAGTTGACCAACTATTTAATCACCGCGCTCAATGGTATT 1593
Qy 690 -----AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal 701
Db 1594 CGCTATGAATCAGTAGGACAACTCCAAACATCTTCTTAATCTGTGATCTGAACCTTAAA 1653
Qy 702 GluGluGluValValGluGluMetMetMetMetMetMetMetMetMetMetMetMetMet 721
Db 1654 CCAGACAGTACCGGTGATGAT-----CAACGCAAGCGGTTTAA 1692
Qy 722 LysLeuIlePheGluGluAsnGlySerIleValProArgAlaCysLysAspAlaPheTyr 741
Db 1693 AAACGCGGTTTTCAGTTAAAGCCAGT----- 1719
Qy 742 AsnMetCysHisValLeuAsnPhePheTyrAlaAsnAspAspGlyPheThrGlyAsnThr 761
Db 1720 GAGTTGTATCAGATGTTATTGATCAGTATCGTAAAGACGCGTGTATCAAAATAAC 1779
Qy 762 IleLeuAspThrValLysAspIle 769
Db 1780 ---TTAGAGAATTGTCTGATCTG 1800
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RESULT 2

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US-11-108-172-1125
; Sequence 1125, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121-471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1125
; LENGTH: 3919
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-108-172-1125

Alignment Scores:
Pred. No.: 0.00437 Length: 3919
Score: 137.00 Matches: 161
Percent Similarity: 35.6% Conservative: 136
Best Local Similarity: 19.3% Mismatches: 300
Query Match: 3.3% Indels: 238
DB: 12 Gaps: 41
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US-10-041-018-383 (1-784) x US-11-108-172-1125 (1-3919)

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Qy 87 AsnTrpLeuIleAsnAsnGln-----LeuAsnAspGlySerTrpGlyLeuVal 102
Db 69 AACCGCTTAATTAGTAACCCAGGAAGCCTTTGTGATTGGAGACGCGCACGGTGGATTACAG 128
Qy 103 AsnHisThrHisAsnHisAsnHisProLeuLeuLeuAspSerLeuSerSerThrLeuAla 122
Db 129 AAGTAC---CAGTCCAAGCAAGAGGAATTACAGAGAGATATCAAGAGGAGTACACAGCA 185
Qy 123 CysIleValAlaLeuLysArgTrpAsnVal-----GlyGluAspGlnIle 137
Db 186 ATGGAAGAATAATAGTCGGAACACAGAACTCTTTTAAAGAGAGCGGTGACGAGTTGTCC 245
Qy 138 AsnLysGlyLeuSerPheIleGluSerAsnLeu-----AlaSer 150
Db 246 CAAGCGGATAGAGCTTTGATTGAGCAGAACTGAAACGAGGTGAAGATGAAGTGTGCCAG 305
Qy 151 AlaThrGluLysSerGlnProSerProIleGlyPheAsp----- 163
Db 306 CTCAACTTAAAGCTGAGCAGTTCGAGAAAGAGTGGATAAGGCAGTGACTACGGCCTC 365
Qy 164 -----IleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAsp 177
Db 366 AAGGAGGAGACTGAAAAGGTTGCGAGTGTGAGGCGAGCTGGAAGAGACAAACCAAGATA 425
Qy 178 IleAsnLeuLeuSer-----LysGlnThrAspPheSerLeuMetLeu 191
Db 426 GAAATCTTTTGAACCTGGTGTCAAATGTTGAGAGAGACTCCGAGGGGTGTGGACCAAG 485
Qy 192 HisLysArgGluLeuGluGlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAla 211
Db 486 CACACACACCCATGAGCAGCAGAACCAACCTATTTCATGAAGGTGATAGCAAGTTAGGA 545
Qy 212 TyrIleSerGluGly-----LeuGlyAsnLeuTyrAspTrpAsn----- 224
Db 546 GCTGCGCAAGAGAGGATGAAGTCAATGTTAACTCTCTGGAGACATGCTGAAGGCGACAGT 605
Qy 225 -----MetValLysLysTyrGlnMetLysAsnGlySer 235
Db 606 GAGGCCACGAGGGGAATCTGAACACGACAGTATGAGAAAGTCAAGGCCCGACGCGAAG 665
Qy 236 ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 666 ATCATGGCTCAGCACCGCGGCTCTTAGCCACGACGCTCGGCCCCAG----- 713
Qy 256 LeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrPro 275
Db 714 -----GTGCTGCTTGAGAAACAGGGCCACTATCTGTCC-----CCC 749
Qy 276 HisAsp-----LeuPheIleArgLeuSer 283
Db 750 GAGGAGAAGGAGAGAGCTGCGAAGAGACACCGCAGAGCTGAAGGTGCATTTAGGAAGGTG 809
Qy 284 MetValAspThrIleGluArgLeuGlyIleSerHisHisPheArgValGluIleLeuAsn 303
Db 810 CTGCGCGAGTGCAGAGAAGAGTGAAGCTCAGCCACTCCCTCCCTGCGAGGAGGAGCTGGAGAAG 869
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1171 AGTATTATAAAGACTTTTCAAAGCAAGTGGACATTTGGGAATGCTGGGTGGCCAGCG 1230
135 ---AspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGlu 153
1231 CTTGATATGGAAGTGAAGGAAGTCAATTTCGTTTAGAACTTTAGAAATCAATTCATGAA 1290
154 LysSerGlnProSerProIleGlyPheAspIle----- 164
1291 ACTAAGACAGCGCGCTTTACTAAATTTTTCAGTTATGGCTGCGGTAGACATTCGTCAAAGTA 1350
165 -----IlePheProGlyLeuLeuGluTyrAlaLysAsnLeu----- 176
1351 GAACAAAATATTGCTAAGAAATTTAGATGAATTTAGTCATCAITTTAGGAATGATGTTTCAA 1410
177 -----AspIleAsnLeuLeuSerLysGlnThrAsp 186
1411 ATTAAAGATGATTTACTGGATGGTATGGTGATGAATCAAACTTGGCAAAAAGTAGGC 1470
187 PheSerLeuMetLeuHisLys-----ArgGluLeuGluGln 198
1471 AGTGATATAGTAATCATAAAGTACTTATGTTTCTTCTTACTTGGAAAAGAGGAGCAGAA 1530
199 LysArgCysHisSerAsnGluMetAspGlyTyrLeuAla----- 211
1531 GAAAGTTAAACAATCATCAA-----TATCTTGTGATGAACCTGCTTAAATCAAAAT 1581
212 -----TyrIleSerGluGlyLeuGlyAsnLeuTyrAsp-----TyrAsn----- 224
1582 TCTGATCAATATGATACTTCTGNAATTAAGTGATATTGTAGATTATCTTCAACAGAGAC 1641
225 -----MetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSerAla 242
1642 CATTAATTTATAAAAAATAT-----ACTATATTAGAATGTCTATTTTA 1686
243 ThrAla-AlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLe 262
1687 ACGTTATAACGCATTTATA-----TCTATAGGTGTCTTCTAGCTTA-----TCTAT 1734
262 uLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspPheIleArgLe 282
1735 GAGGCAATCTTTT-AAATCT-----TCAATTTATATACAAGAATTATTCACATTTT 1787
282 uSerMetValAspThrIleGluArgLeuGlyIleSerHisPheArgValGluLeu 302
1788 ATTCTTA----- 1794
302 sAsnValLeuAspGluThrTyrArgCysTrpVal-----GluArgAspGluGlnIlePh 320
1795 -----AACACTTATTTTATAGTATTATTAATTTAGGAATGATTTTGTATAATAA 1841
320 eMetAspValValThrCysAlaLeuAlaPheArgLeuLeuAlaGlyIleAsnGlyTyrGluVa 340
1842 TACTGATATAGT-----CTCGTTAGATATTTTAACTTTACAT 1880
340 lSerProAspProLeuAlaGluIleThrAsnGluLeuAlaLeuLysAspGluTyr----- 358
1881 TTCAAAAATAGTGTGTAGTAGTCTCAGAACTCCATGTG-TTAAATCAATGATATAATA 1939
359 -----AlaAlaLeuGluThrTyrHisAlaSerHisIleLeuTyrGlnG 373
1940 TTCGTAATTTGAGGTGTTAATGTCGCAAAAAAGTCAGTGAGACATATAAAAAATAAGAGA 1999
373 uAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleLeSe 393
2000 G---ATAATTTCAAATGAACAATAGAACACACAGATGAAGTATTAAAGTTTGAATGA 2056
393 rThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGlu-----AsnAlaLe 411
2057 GTATGATTTAAATGTTACACAGCTACTGTTTCCAGCAGATATTATAAGAAATTTGCAATTAAT 2116
411 uLysPheProIleAsnThrGly----- 418

2117 TAAAGTTCTCTGCACCTACAGGCAATATGTTTATAGTTTACCAAATGATCGTAGATATCA 2176
419 ---LeuGluArgIleAsnThrArgAsnIleGlnLeuTyrAsnValAsp----- 434
2177 TCCATTAGAGAAGTTGGGTAGATATTAAATGATGATTCATTTGTTAAACATTTGAGGCTACTGG 2236
435 -AsnThrArgIleLeuLysThrThrTyrHisSerSerAsn-----IleSe 449
2237 TAACTACTAGTCTTTAAACGCTTCTCCTGGTAAATGCTCAATCCATCTGGTGTCTATCTTGA 2296
449 rAsnThrAspTyrLeuArg-----LeuAlaValGluAspPheTyrThrCysG 465
2297 TCAAAATTGATGGGATGAGTACTTGGTACAAATTTGCTGGTGATGAT-----ACATGCTT 2350
465 nSerIleTyrArgGluGlu-----Le 472
2351 ACTTATTTGTCGACGACGAAGAAGCGAGTGAAGAAATCAAAACTCGAAATTTTCAATTTAT 2410
472 uLysGlyLeuGluArgTTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArg 492
2411 ATAAGATCGCAATGAAATTTATGTTTACAAACC---TTATCAATAAAACAATTTGCCATTTAT 2467
492 nLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAs 512
2468 TCACGNACTTGATATAAACTTTTCTGACGCTTAACAGTTATGAGTGTGGAACGCTC 2527
512 p-----AlaArgIleSe 516
2528 AGGAAAACTCTATCATTTATGATGCCATTTGACAGCTTAATCGGTATGAGAGCTTCTTCTGA 2587
516 rTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyL 536
2588 TTACGTCGACATGTTGTAAGAAAGCAATTTCAAGAGGTATCTTTGAT----- 2636
536 rIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspL 556
2637 -ATAGACGAGATAAGAGCAATTAATATACAGTATCATAGTATAGATGTTGATGA 2695
556 sAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLys----- 571
2696 AGAT-----TTTTTATTAGTTAAAGAGAAATTTTTCAG 2728
572 -----AspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspVa 589
2729 TTTCTGTAAGATGATTTTTCGTATTATAAACCAACTGCTCACTCTACAG-----GACTT 2782
589 lThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAla 609
2783 AAGAAAA---GTGATGCAAGAACTGCTTGATATTTCATGCTCAACATGAACGCAATCTTT 2839
609 eTrpThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSe 629
2840 ACTTAAGCAAAAATATCATCTTCAACTATTAGATGATTATGACACAATCAGTATTTCAGA 2899
629 rPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerG 649
2900 TTTA-----CTTAATCA 2911
649 uGluIleValGluSerSerGluTyrHisAsn-----LeuPheLysLeuMetSe 665
2912 ATATCACTTTCTTATAACCAATATAAAATAAAGTAAAGAAATTAGAGAAATTAGAAATC 2971
665 rThrGlnGlyArgLeuAsnAspIleHisSerPheLysArgGluPheLysGluGly 685
2972 CGCGGACCAAGGCTTTTATTACAAGATTAGACTTAATGAAATTTCAATTTAGAGAA----- 3026
685 sLeuAsnAlaValAlaLeuHisLeuSerAsnGlyLeuSerGlyLysValGluGluVa 705
3027 -----CTAACCGAAGCTTCTGAAGAGCGGAAGTGGACCAACTTGAATCCCATAT 3079
705 l-----ValGluGluMetMetMetIleLysAsnLysArgLysGluLe 720
3080 TAAAGAAATTCAAAACTCCGAAAAAATAAATCTAGCTTTTAAACAATGCATCAAGTTCT 3139

QY 720 uMetLysLeuIlePheGluAenGlySerIleValProArgAlaCysLysAspAlaPh 740
Db 3140 A-----ACTGATGAAGTGCATATACC-----GATAGTT 3169
QY 740 eTrpAsnMetCysHisValLeuAenPhePheTyrAlaAsnAspGlyPheThrGlyAs 760
Db 3170 GTACGAATTA-----AG 3181
QY 760 nThrIleLeuAspThrValLysAspIleIleTyrAsnProLeuValLeuValAsnGluAs 780
Db 3182 CACTACTTGCACACGATTATGATATCGTTCCAGAAAAATTCGTAGATTAAAGAGGA 3241
QY 780 nGluGluGln 783
Db 3242 CATTGATCAA 3251

RESULT 6

US-11-052-554A-514
; Sequence 514, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 514
; LENGTH: 3735
; TYPE: DNA
; ORGANISM: Mycoplasma pneumoniae
US-11-052-554A-514

Alignment Scores:

Pred. No.: 0.072 Length: 3735
Score: 125.00 Matches: 186
Percent Similarity: 34.1% Conservative: 137
Best Local Similarity: 19.6% Mismatches: 338
Query Match: 3.0% Indels: 286
DB: 12 Gaps: 45

US-10-041-018-383 (1-784) x US-11-052-554A-514 (1-3735)

QY 37 ProThrAsnLeuIleAspThrThrLysGluArgIleGlnLysGlnPheLysAsnVal 56
Db 91 CCTTCAACTCGCGTTTACAAACGGTTTAAAGCGGTTCCAGTCAGTGTTCATGGT 150
QY 57 GluIleSerValSerSerTyrAspThrAlaTyrValAlaMetValProSerProAsnSer 76
Db 151 GAA-----CAGGGTAGTTTACAAAGTCCCTAACACGGCTTTAAAAATCCAGTGGCC 204
QY 77 ProLys-----SerProCysPheProGluCysLeuAsnTyrLeuIleAsnAsn 92
Db 205 AACAAACAAATTTATCGCTGCACCACTTTTAAAGCACTAGAACGTTGGTACGAAACAAAC 264
QY 93 GlnLeuAsnAspGlySerTyrGlyLeuValAsnHisThrHisAsnHisAsnHisProLeu 112
Db 265 GAA-----GACAAAAGATTATCCAGTTT 288
QY 113 LeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTyrAsnVal 132
Db 289 TTAAGACACACTAAGTCCATGTTGACAGT-----CAGTACACACG 330
QY 133 GlyGluAspGlnTle-----AsnLysGlyLeuSerPheIleGluSerAsn 147
Db 331 GCAGTCGATAAAGTGGTATCAGCATCAGCGCAATAAATCACTT---TTTGTGCAACAAGAT 387

QY 148 Leu-----AlaSerAlaThrGluLysSerGlnPro----- 157
Db 388 TTGTTGGATAACCGCGTGTAGTGAAGCAACTGGNAAGCGCAAAAGCTGCTTGAACAG 447
QY 158 -----SerProIleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsn 175
Db 448 CTCATTAGTGACTTTGCTAGTCGGGTTTCCAAAAGAACTACCTCAATTACAAAAGAGAT 507
QY 176 LeuAspIleAsnLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGlu 195
Db 508 GGACAAGTTTCTACTGCTCCATTACTATGAT-----GAACTACACNAGGAAGAA 558
QY 196 LeuGluGlnLys----- 199
Db 559 AGCTGAAAAAACTTTGNAATTTAGTGCCCAAGTTTGTAGTGAACAACTAATGATGACTTTTTC 618
QY 200 ---ArgCysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIle----- 213
Db 619 GCCAAAATTCAAAGCCCAAGTATTGACCAATGGGTGGAGTACACTGATCCCACTTTAATT 678
QY 214 -----SerGluGlyLeuGluAsnLeuTyrAspTyr 223
Db 679 AGTCAAGTTAACTATAAGTATTCTGCTCCAGTCAAGGGTTAGGTTCAGATCTATAACAGA 738
QY 224 AsnMetValLysLys----- 228
Db 739 GAGAAGTTAAAGGATAAATAACACCTTCTATGCTTCTTCTTTCGCGAAGAAAAA 798
QY 229 -----TyrGlnMetLysAsnGlySer 235
Db 799 GACATTGCAACCCCAACAAACGTTGGTAAAGCGCTGAAAGCAGTTTGTATTAAGGTGAG 858
QY 236 valPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 859 GCGCTATTACTGATAATAATATCGGTCAAAGCGGTACAAACAGCCCAACAACTGGTCTG 918
QY 256 LeuAsnTyrLeuAsn-----SerLeuLeuAspLysPheGlyAsnAlaVal 270
Db 919 CTCAAATACGGTAAATCAATCAATAGGGTGATTTCTTGATTTTCCCTTAATTTATCA 978
QY 271 ProThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGlu--- 289
Db 979 GATACTAAACGAAAGCAATTTAGTAGACGCTTCTTAACATTTGCGATCAGTTAGAAGCT 1038
QY 290 ---ArgLeuGlyIleSerHisPheArgVal----- 299
Db 1039 GCTAACTTAGTGCAGCTTTAAATTTAAAACTGCAAGTTTTCGACGAAGATAATGACGAA 1098
QY 300 -----GluIleLysAsnValLeuAspGluThrTyrArgCysTyrValGlu 314
Db 1099 TTGCCCAATTAAGAGAGCTCAAAAGAACCTTTACACACG-----ATTGTTGTCAT 1152
QY 315 ArgAspGluGlnIlePheMetAspValThrCysAlaLeuAlaPheArgLeuLeuArg 334
Db 1153 AAAAGTAAGGACGTAGAAAAAGCTTCCAAAACCTAACGCACTGTTTACATATGATCAAGAA 1212
QY 335 IleAsnGlyTyrGluValSerProAspProLeuAla----- 346
Db 1213 GGTAAGCAACAACAAAGTGAAGTCAATGCTGCGCTTTAGATGACATTTTGTGCT 1272
QY 347 -----GluIleThrAsn-----GluLeuAlaLeuLysAspGluTyrAlaAla 360
Db 1273 CAAAACACAGCGNAGCGCTAACTTAAGTAAGTTAGCGGAGCGGTGAAGAAAGAGAGCT 1332
QY 361 LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLysGln 380
Db 1333 GCACAAAATGGAAGCGAAACAGCTGTTTAAAGAACTAAACAATTTCTAAGGGCCCAACAA 1392
QY 381 -----IleLeuLysSerAlaAspPheLeuLysGluIleLeuSerThrAspSer 396
Db 1393 AACAAATTAGCTTTGTTTATAGTCAGCT-----ATTCTACATTTAAT 1434


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; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793.626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3667
; LENGTH: 3729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3667

Alignment Scores:
Pred. No.: 0.166 Length: 3729
Score: 121.50 Matches: 174
Percent Similarity: 31.4% Conservative: 133
Best Local Similarity: 17.8% Mismatches: 305
Query Match: 3.0% Indels: 367
DB: 8 Gaps: 44

US-10-041-018-383 (1-784) x US-10-793-626-3667 (1-3729)

QY 4 SerLeuCysIleAlaSerProLeuLeuThryLysSerAsnArgProAlaAlaLeuSerAla 23
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3616 AGCGTTCAATATCTAATCAATATATCTGCTTAAACGAGACAGAAAGTTGCCAAGCA 3557

QY 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3556 ATTGAAAAGCAAAATCA-----TTAAAT 3533

QY 44 ThrThryLysGluArgIleGlnLysGlnPheLysAsnValGluLysSerValSerTyr 63
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3532 CATGCAATGAAGCATTAAACAAATATATATAAAATGCAGATAAAGTTAGATAGT--- 3476

QY 64 AspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPhePro 83
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3475 -----AGTCGATTCTTAACGAGATCAACTCGAAACAGCTCAAAATTAACATTTACATGGTGAT 3431

QY 84 GluCysLeuAsnTrp-----LeuIleAsnAsnGlnLeuAsn---AspGlySerTrp 99
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3430 CAAGTATAAATCATGTGTTGATTCAATCATTCATAGACAAACAAATCTCGAATGGATCCA 3371

QY 100 GlyLeuValAsnHis---ThrHisAsn-----HisAsnHis 110
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3370 ACAGTATCAATAGCATCACTCACTGAACCTCGAAACAGCTCAAAATTAACATTTACATGGTGAT 3311

QY 111 ProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrp 130
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3310 CAGAAACTTCTGCTCATGCAAAACAGATGCGCTAATGTAATTAATGCTCTAATTCATCTT 3251

QY 131 AsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSer 150
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3250 AATGTTGCTCAACCGAGTA-----ATGATAAATAGCAATACAAATGCT 3206

QY 151 AlaThrGluLysSerGlnProSerProIleGlyPheAspIlePheProGlyLeuLeu 170
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3205 ACAACACCGCAA----- 3194

QY 171 GluTyraLysAsnLeuAsp---IleAsnLeuLeuSerLysGlnThrAspPheSerLeu 189
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3193 AAAGTTGCAAGAACTTAGATAATGCTCAAGCTCTTGATAAAGCTATGGAA----- 3143

QY 190 MetLeuHisLysArgGluLeuLysArgCysHisSerAsnGluMetAspGlyTyr 209
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3142 -----ACATCAACAAAGTAGTGTCTCATATAAATAATATATATTGAAGCAT 3098

QY 210 LeuAlaTyrlSerGluGlyLeuGlyAsnLeuTyraPheAsnMetValLysLysTyr 229
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3097 AGTAAATATTAAATGAAGAT-----TCAAAATAT 3068

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QY 230 GlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsn 249
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3067 CAACAACAATACGATCGATTAT-----GCTGATGCCGACAACACTACTTAAT 3020

QY 250 His---GlnAsnProGlyCysLeuAsnTyLys-----AsnSerLeu 262
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3019 CAGACAACAATCCAACTTAGAACCTTATAAAGTCGATATTGTTAAGGATAATGTCCTA 2960

QY 263 LeuAspLys-----PheGly-----AsnAlaVal 270
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2959 GCTAAACGAAAAATACTATTGTCGCGCAGAAAAAACTATCATATGCAAAATCAAAATGCAAAAT 2900

QY 271 ProThrValTyxProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArg 290
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2899 GATGAATTT---AAACATATGAATTTATCTTAATAATGCACAAAAGCAATCTATAAAGAT 2843

QY 291 LeuGlyIleSerHis---HisPheArgValGluIleLysAsnVal----- 304
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2842 ATG---ATTTCTCAGCGCAGCATTTAAGAACTGAAGTTAAACAACTTCTGCAACAGCTAAA 2786

QY 305 ---LeuAspGluThrTyxArgCysTrpValGluArgAspGluGlnIlePheMetAspVal 323
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2785 ACCCTTGATGAAGCTATGAATCACTTGAAGATAAAACTCAAGTAGTGTATTACAGATACT 2726

QY 324 Val-----ThrCys 326
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2725 ACTTTCGCTTAATTACACTGAAGCTTCAGAGGATAAAAGAAAAAGTAGACCAACTGTGA 2666

QY 327 AlaLeuAlaPheArgLeuLeu---ArgIleAsnGlyTyxGluValSerProAspProLeu 345
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2665 TCACATGCTCAAGCAATCATTTGATAAAATAAATGCTCAAAATGTAAGTTTAGATCAAGTA 2606

QY 346 AlaGluIleThrAsnGluLeuAlaLeuLys-----AspGluTyxAla 359
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2605 CGACAAGCAGCTAGAACAAATTAACCAAGCATCAGAAAAACCTCGATGCTGATCAGCGAGTT 2546

QY 360 AlaLeuGluThrTyxHisAlaSerHisIleLeuTyxGln---GluAspLeuSerSer--- 377
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2545 GAAGAAGCTAAAGTTTCATGCTAATCAACAAATTAACCAATTAACACACTTCTTAATTCATTA 2486

QY 378 -----GlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleIleSer 393
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2485 CAACAACAACCTCGAAAGAAAGTGTTAAAAACGCAACAACTAGAGAAGAAATCGCTACT 2426

QY 394 ThrAspSerAsnArgLeu----- 399
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2425 GCTAGTAACAATGCTCTGCGCATTTAAACAAAGTAATGGTAAATTAGAACAAATTCATTAAT 2366

QY 399 ----- 399
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2365 CATGCTGATTCTATTGAAAATAGTGATAATTATAGACAGCCGACGACGACAAATATATC 2306

QY 400 -----SerLysLeuIleHisLys 405
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2305 GCTTATGATGATGCTAGCACTAGAACATGCGCAAGATATACAAAAATCTAACGCAACCCAAAT 2246

QY 406 GluValGluAsnAlaLeuLysPheProIleAsn-----ThrGlyLeuGlu 420
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2245 GAAGCAAAAACAGCGTTACAACAATTAATAAATGCAGAAACACATCGTTAAATGGTTTCGAA 2186

QY 421 ArgIleAsn----- 423
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2185 AGATTAAATCATGCTAGACCCAGCGCTTTAGAAATATATTAATCACTAGAAAAAATAAAC 2126

QY 423 ----- 423
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2125 AATGCTCAAAAGCTCTCTTTAGAGGATAAAGTAACCGCAATCGCATGTTTATTAGATTA 2066

QY 423 ----- 423
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2065 GAACATCTTGTCAACGAGGCGCAACAACTCAATGACATTTATGGTGAATTAGCTAACGCA 2006

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QY 424 -----ThrArgAsnIleGlnLeuTyrAsnValAspAsnThr 436
Db 2005 ATGTTAAATACTATGCTCAACCAAGCAAGATATAATATATTAAACCGCATACCTA 1946
QY 437 ArgIleLeuLysThrTyrHisSerSerAsnIle----- 448
Db 1945 CGCAAGATAACTTTACTCAAGCTATCAACATGACGTCATGACCTCAACAAACTCAA 1886
QY 449 ---SerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIle 467
Db 1885 GGTCAAGAACTTAGATTTC-----AATGCAATTGATACATTTAAAGATGATATATTTCAA 1832
QY 468 TyrArgGluGluLeuLysGlyLeuGluArgTTPVal-----ValGluAsn 482
Db 1831 ACTAAAGATGCACTTAAACGGTATTGAACGTTTAAACAGCTGCAAAATCAAAAGCAGAAA 1772
QY 483 LysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAla 502
Db 1771 CTAAATTGATGTTAAATTT----- 1751
QY 503 AlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsnGlyIle 522
Db 1750 -----ATTAATAAAGCTCAATTCACATGCAATGATGAAAT 1712
QY 523 LeuThrThr-----ValValAspAspPhePheAspIleGly 534
Db 1711 ATGAATACTAATTTCTATTGTCACAATTTGCTAGATCGTGAATCAAGCATTTGATTTAAAT 1652
QY 535 GlyThrIle-----AspGluLeuThrAsnLeu-----IleGlnCysVal 547
Db 1651 GATGCAATGAATCTTTAGAGATGAACTTAATATCAAGCTTTCTCTCCAGCAAGC 1592
QY 548 GluLysTrpAsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPhe 567
Db 1591 TCAAAATTAAT-----ATAAATTCAGATGAAT----- 1565
QY 568 LeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArg 587
Db 1564 -----TTAAACCAACAATTTGACCATGCTTTAAGTAATGCTCGAAAGACTCTTGCAAA 1511
QY 588 AspValThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGlu 607
Db 1510 GAAATGTTAAATTTAGATGAAATACAAATGAGGGACTCAACAAAGTATGAGGAT 1451
QY 608 AlaIleTrpThrArgAspAla----- 614
Db 1450 -----ACTAAGATGCTTTAAATGGTATCTCAACGTTTATCAAAAGCTAAAGCTAAA 1400
QY 615 -----TyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAla 631
Db 1399 GCAATTCATACGTACAATCTTTA-----TCTTATATCAATGATGCA 1358
QY 632 LeuGlyProIleValLysProAlaIleTyrPheValGly-----ProLysLeuSerGlu 649
Db 1357 CAGCGTCATATTGCTGAAGATTAATTCACAACTCTGATGATTATCATCTTTAGCAAT 1298
QY 650 GluIleValGluSerSerGluTyrHisAsnLeuPheLys-----LeuMet 664
Db 1297 ACATTATCTAAAGTAGTGTAGTATAATGCAATGAAAGACTTACGAGATCTCTAGAA 1238
QY 665 SerThrGlnGlyArgLeuLeuAsnAspIleHis-----SerPheLys 678
Db 1237 AGTAATTCACCTTCTGTTCCAAATAGTGTGAATTTATTAATGCTGATGAATTTACAA 1178
QY 679 ArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSer 698
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QY 699 GlyLysValGluGluValVal----- 706
Db 1117 CCAGCAACGATTGCAAGAGTATTAGTCTTAGTCAAGCCATTTACGATACAAAAATGCA 1058
QY 707 -----GluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLys 722
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Db 1057 TTGAATGGTGAACAACAGCTTTCCAACTGAGAAGACCAAGATTAAATTAATAAAA 1001
RESULT 10
US-10-947-249-105
; Sequence 105, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: AKIRA NAKAGAWARA
; APPLICANT: MIKI OHIRA
; APPLICANT: SHIN ISHII
; APPLICANT: TAKESHI GOTO
; APPLICANT: HIROYUKI KUBO
; APPLICANT: TAKAHIRO HIRATA
; APPLICANT: YASUKO YOSHIDA
; APPLICANT: SAICHI YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 6773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-105
Alignment Scores:
Pred. No.: 0.37 Length: 6773
Score: 121.50 Matches: 117
Percent Similarity: 34.0% Conservative: 100
Best Local Similarity: 18.3% Mismatches: 208
Query Match: 3.0% Indels: 213
DB: 8 Gaps: 28
US-10-041-018-383 (1-784) x US-10-947-249-105 (1-6773)
QY 113 LeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnVal 132
Db 416 CTGGAAGAGCAATGATACGCAATTAGAATTTTTCAGAACAACTTAATTTTCAAGAACAC 475
QY 133 GlyGluAspGlnIleAsnLys----- 139
Db 476 TCTGAAGATAATGTTTAAATAAACTCAAGAAGAGATTGAGAAAAATTAGGCCAGCTTTGAG 535
QY 140 ---GlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSer 158
Db 536 GAGCAAAATTTTATATCTGCAAAAGCAATTAGACGCTACCACTGATGAAAGAGGAACA 595
QY 159 ProIleGlyPhe---AspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAsp 177
Db 596 GTTACTCAACTCCAAATATCATTTGAGGCTAATTTCTCAGCAATTTACAAAAAATATATAT 655
QY 178 IleAsnLeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlu 197
Db 656 -----AGTTTCAGGAGAGAGCTTTTACAG 679
QY 198 GlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIleSerGluGlyLeu 217
Db 680 TTGAAAGCTTATACACCAAGAGAGGTGAAAGAGTTGATGTGCCAGATTGGAAGCATCA--- 736
QY 218 GlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPhe 237
Db 737 -----GCTAAGCAACATGAAGCAGAG----- 757
QY 238 AsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsn 257
Db 758 -----ATAAAT 763
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Qy	258	TyrLeuAsnSerLeuLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAsp	277
Db	764	AAAGTTGAACGAGCTTAAAGAGAACTTA	790
Qy	278	LeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHisphe	297
Db	791	-----GTAAACAATGTGAGCAAGTCAAAAG--AACATCCAGAGAATAAT	835
Qy	298	ArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAspGlu	317
Db	836	GAATGTGAGTTAGAAAAATTTAAGAAAGGCCACCTCAAAT-----GCAACCAAGACACAAT	889
Qy	318	GlnIlePheMetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGly	337
Db	890	CAGATA-----TGTTCTATT-----CTCTTGCAGAAAAATACA	922
Qy	338	TyrGluValSerProAspProLeuAlaGluIleThrAsnGluLeuAla-----LeuLys	355
Db	923	TTT-----GTAGAACACAGTAGTAATGAAAAGTCAACACCTTAGAA	964
Qy	356	AspGluTyrAlaAlaLeuGluThrTyrHisAla-----SerHisIleLeuTyrGln	372
Db	965	GATACCTTAAAGAACTTGAATCTCAACACAGTATCTTAAAGATGAGGTAACTTATATG	1024
Qy	373	GluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleIle	392
Db	1025	AATAAT-----CTTAAGTTAAAACTT	1045
Qy	393	SerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLys	412
Db	1046	GAATGATGCTCAACATATAAAGATGAGTTTTTTTCATCAACGGGAAGAC---TTAGAG	1102
Qy	413	PheProIleAsnThrGlyLeuGluArgIleAsnThrArgAsnIleGlnLeuTyrAsn	432
Db	1103	TTTAAATTAATGAA-----	1117
Qy	433	ValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsnThrAsp	452
Db	1117	-----	1117
Qy	453	TyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGluGluLeu	472
Db	1118	---TTATTACTAGCTAAAGAAGAACACAGGCTGTGTAATTGAAAATAATTAAATCTGAGCTA	1174
Qy	473	LysGlyLeuGluArg-----TrpValValGlu-----AsnLysLeuAspGln	486
Db	1175	GCAGGTTTAATAAACACAGTTTTTGTCTATCTGTAGACAGCATACAGAGAATGACAGT	1234
Qy	487	LeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSer	506
Db	1235	CTTAAGGAACAACATCAAAA-----GAA	1258
Qy	507	SerProGluLeuSerAspAlaAraArgIleSerTrpAlalysAsnGlyIleLeuThrThrVal	526
Db	1259	ATATCAGAACTAAATGATGACATTTTGTCTGATTCAGANAAAGAAAAATTTAAACATTAATG	1318
Qy	527	ValAspAspPhePheAspIleGlyIleThrIleAspGluLeuThrAsnLeuIleGlnCys	546
Db	1319	-----TTTGAATAACAGGCTCTTAAGAACACAGTGTGNAACCTCAGCAA---	1363
Qy	547	ValGluLysTrpAsnValAspValAspLysAspCysCysSerGluHisValArgIleLeu	566
Db	1364	---GAAAAGCAAGAAGCAATTTTAAATATGAGAGATTTACGAGAGATTATGGAAATTTTA	1420
Qy	567	PheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGlu-----AlaPheLys	583
Db	1421	CAAAACAGAACTGGGGGAATCTGCTGGAAAAAATAAGTCAAGAGTTCGAATCAATGAAGCAA	1480
Qy	584	TrpGlnAlaArgAspValThrSerHisValIleGlnIleThrTrpLeuGluLeuMetAsnSer	603
Db	1481	CAGCAACACTCTGATGTT-----CATGAACTGCAG-----CAG	1513
Qy	604	MetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProThrLeuAsnGluTyrMet	623

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Db      1514  AAGCTCAGAACTGCTTTTACTGAAAAGATGCCCTTCTCGAAACTGTGAATCGCCTCCAG 1573
Qy      624  GluAsnAlaTyrValSerPheAlaLeuGlyProIleValIysProAlaIleTyrPheVal 643
Db      1574  GGAGAAATCAAAAGTTACTATCTCAACAAGATTGGTA----- 1612
Qy      644  GlyProIysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeu 663
Db      1613  ---CCGAACTTCAAAATACCAATAAAGAACCTTCAAGAAAAGAAATGGAGTATACTTACTT 1669
Qy      664  ---MetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLys 682
Db      1670  AGTCTCAGTCAAGAGATACCATGTTAAAAGAAATTA----- 1705
Qy      683  GluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGlu 702
Db      1706  GAAGGAAGATAAATCTCTTACT----- 1729
Qy      703  GluGluValValGluGluMetMetMetIleLysAsnLysArgLysGluLeu 720
Db      1730  ---GAGGAAAAGAGATGATTTTATAAATAAACTGAAAAAATTCCTCATGAAGAAATG 1780

RESULT 11
US-10-793-626-2963
; Sequence 2963, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2963
; LENGTH: 15071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2963

Alignment Scores:
Pred. No.: 1.09 Length: 15071
Score: 121.50 Matches: 174
Percent Similarity: 31.4% Conservative: 133
Best Local Similarity: 17.8% Mismatches: 305
Query Match: 3.0% Indels: 367
DB: 8 Gaps: 44

US-10-041-018-383 (1-784) x US-10-793-626-2963 (1-15071)
Qy      4  SerLeuCysIleAlaSerProLeuThrLysSerAsnArgProAlaAlaLeuSerAla 23
Db      10099  AGAGTTTCATATCTAATCAATATATATCTGTAAACGAGAACACAGAAAGTCCCAAGCA 10158
Qy      24  IleHisThrAlaSerThrSerHisGlyGlnThrAsnProThrAsnLeuIleLeuAsp 43
Db      10159  ATTGAAAAGCAAAATCA-----TTAAAT 10184
Qy      44  ThrThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTyr 63
Db      10183  CATGCAATGAAGACACTTAACAAATATATAAAATGCGAGATAAAGTGTAGATAGT--- 10239
Qy      64  AspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPhePro 83
Db      10240  -----AGTCGATTCATTACGAAGATCAACCTGAAAAAGAGCGGTATCA 10284
Qy      84  GluCysLeuAsnTrp-----LeuIleAsnAsnGlnLeuAsn---AspGlySerTrp 99

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QY 608 AlaIleItrpThrArgAspAla----- 614
Db 12265 -----ACTAAGATGCTTTAAATAGGTATCCAAGTTTATCAAAAGCTAAAGCTAAA 12315
QY 615 -----TyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAla 631
Db 12316 GCAATTCAATACGTACAACTCTTTA-----TCTTATATCAATGATGCA 12357
QY 632 LeuGlyProIleValLysProAlaIleTyrPheValGly-----ProLysLeuSerGlu 649
Db 12358 CAGCGTCATATGCTGAAAGTAATATTCACAACTCTGATGATTTATCATCTTTAGCAAAAT 12417
QY 650 GluIleValGluSerSerGluTyrHisAsnLeuPheLys-----LeuMet 664
Db 12418 ACATTATCTAAGCTAGTGAATTTAGATATGCAATGCAATGAAAGACTTACGAGATCTCTAGAA 12477
QY 665 SerThrGlnGlyArgLeuLeuAsnAepIleHis-----SerPheLys 678
Db 12478 AGTAATTCAACTTCTGTCCAAATAGTGTGAATTTATATTAATGCTGATAAGAAATTTACAA 12537
QY 679 ArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSer 698
Db 12538 ATTGAATTTGATGAGCGCTACAAACAGCAAGTGCACAAAGTTCTTAAACTTCAGAAAT 12597
QY 699 GlyLysValGluGluGluValVal----- 706
Db 12598 CCAGCAACGATTGAAGAAATTTAGGTCTTAGTCAAGCCATTTACGATACAAAATATGCA 12657
QY 707 -----GluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLys 722
Db 12658 TTGAATGGTGAACAACGCTCTGCAACTGAGAGGAGCAAGATTTAAATTAATAAAA 12714

RESULT 12
US-10-793-626-3375/c
; Sequence 3375, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: FU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3375
; LENGTH: 3146
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3375

Alignment Scores:
Pred. No.: 0.148 Length: 3146
Score: 121.00 Matches: 126
Percent Similarity: 34.3% Conservative: 105
Best Local Similarity: 18.7% Mismatches: 223
Query Match: 2.9% Indels: 221
DB: 8 Gaps: 27

US-10-041-018-383 (1-784) x US-10-793-626-3375 (1-3146)

QY 174 LysAsnLeuAspIleAsnLeuLeuSerLysGln----- 184
Db 2924 AGACAACCTGACTTAACTAGCTGCGAAAAGAAAGTAAGCGCTCTCTTTATATAGTGTG 2865
QY 185 -----ThrAspPheSerLeuMetLeuHisLysArgGluLeuGlu----- 197
Db 2864 AATGACTAACCGAGTTTAAATGCAACACAAAGTGAAGCGCTAGAGGAATTGGACCAA 2805
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QY 198 -----GlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAla 211
Db 2804 TTAGGTTTTAAACCTAACCAAGACGTGAACGAGTATCAGATATTGAGGCGGTACTTAAT 2745
QY 212 TyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMet 231
Db 2744 TATATA-----GAGAAATGCAAGC 2724
QY 232 LysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGln 251
Db 2723 AAAAGAGGATCT-----TTATCTTACGAT 2700
QY 252 AsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro 271
Db 2699 ATTGATGGTATTGTTTAAAGTTAACGATTATCTCAACAGA-GGAATGGG----- 2647
QY 272 ThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeu 291
Db 2646 -----TTATACGCAAAAATCTCC-----AAGATG 2623
QY 292 GlyIleSerHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArgCy 311
Db 2622 GCGCATTTGCTTATAAATTTCCAGCTGAA----- 2595
QY 311 sTrpValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPheAr 331
Db 2594 -----GAAGTTATTACAAAATTTATGGTATATGA 2566
QY 331 gLeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGl 351
Db 2565 GCTAAGTATTGGCGTACGGTCTGTGACACCACTGCAATTTCTAGAACCTGTAAAGT 2506
QY 351 uLeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisLeuLeuTy 371
Db 2505 AGCTGGTACTACAGTTTCAAGAGCCCTCACTT-----CATAATGAAGATTTAATACA 2455
QY 371 rGlnGluAspLeuSerSerGlyLysGlnIleLeu-----LysSerAlaAspPheLeuLy 389
Db 2454 TGAAGAGATATACGTATCGAGATAGTGTGTTTATTAAAGAACCCGGGACATCATCCC 2395
QY 389 sGluIleIleSerThrAspSerAsnArgLeu-----SerLysLeuIleHisLysGl 406
Db 2394 TGAAGTTGTAAGAAAGTATTTTAGATAGCAGCACCTAACGAATCGGAATTTATCATATGCC 2335
QY 406 uVal-----GluAsnAlaLeuLysPheProIleAsnThrGlyLeuGl 420
Db 2334 AACACATTGCTCCTAGTTGTGGACATGAATTAGTTGTTGTAAGGAGAGAGTTGCTTTACG 2275
QY 420 uArgIleAsnThrArgArgAsnIleGlnLeu----- 430
Db 2274 TTGTATTAATCCAAATATGTCAGGCACAGCTTATTGAAAGGACTTATACATTTGCTTTCAAG 2215
QY 431 -----TyrAsnValAsp-----AsnThrArgIleLeuLysThrThrTyrHisSerSe 446
Db 2214 ACAAGCGATGAATATAGATGGTTTAGTACTATAAATTTATCATCAGCTATACGNAATCA 2155
QY 446 rAsnIleSerAsn-----ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGl 465
Db 2154 GTTAATCAAGAGATGTCGAGATATTTTCTATTGAAAGAGAAGATTTATTACCATTAGA 2095
QY 465 nSerIleTyrArgGluGluLysGlyLeu----- 475
Db 2094 GCGAATGGGAAAGAGAAGATTTGATAATCTTTTATTAGCGATAGAAAAATCTAAGAACA 2035
QY 475 ----- 475
Db 2034 GTCATTAGACATTTTATTATTGGACTTGGTATTAGACATTTTAGGTGTAAAGCTAGTCA 1975
QY 476 -----GluArgTrp-----ValValGluAsnLysLe 484
Db 1974 AGTACTTGTCTGACCGATATCAAAAGATGGATCAACTTTTTTAAAGTAACCTGAAAGTGAATT 1915
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QY 484 uAspGlnLeu-----LysPheAlaArgGlnLysThrAlaTyrCysTyrPh 499
DB | : : : : :
1914 AATTGAATTCAGATATTTGGAGATAAATCTGCACATCTGTGTAAACATATCTCGAAA 1855
QY 499 eSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLys 519
DB | : : : : :
1854 TAGTGATATTCGTTTCATTAATTGAA--AAATTAAGTAATAAAATGTTAATATGCTTFA 1798
QY 519 sAsnGlyIleLeuThrThrValValAspAspPheAspIleGlyGlyThrIleAspG1 539
DB | : : : : :
1797 TAAAGGAATTAACAACTGAAATCAAGGTCACTGCTGATTTTAGTGGGAAACAAATGTT 1738
QY 539 uLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCy 559
DB | : : : : :
1737 ATTACAGGGAACTCGAGCAATGACGAGA----- 1707
QY 559 sSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAs 579
DB | : : : : :
1706 -----AATGAAGCATCTGAATGTTG----- 1686
QY 579 pGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuG1 599
DB | : : : : :
1685 -----AAAATGCAAGGTGCTAAAGTTACAAGCAGCGTGAATTAAGTACTGATAT 1636
QY 599 uLeuMet-----AsnSerMetLeuArgGluAla----- 608
DB | : : : : :
1635 TGTCAATAGCTGAGCAGATGCGGGTCTAAATAGCCAAAGCTGAGAGTATGGTACTGA 1576
QY 609 -IleTrpThrArgAspAlaTyrValProThr-----LeuAsnGluTyr 622
DB | : : : : :
1575 AATTGGACTGAAGCAGCATTTATTGAAAAACAAATGGAATCTAATAATTAGAGGAGTA 1516
QY 622 rMetGluAsnAlaTyrValSerPheAla-LeuGlyProIleValLysProAlaIleTyrP 642
DB | : : : : :
1515 CGTGAATGAAGCAACAATATTTTACTCATCTCGATATCTGTTATTTAAACGGCTTGG 1456
QY 642 heValGlyProLysLeuSerGluGluIleValGluSerSerGluTyr----- 657
DB | : : : : :
1455 GAGATGGACATAAACAATCTCATCAGATAAAGAACAAAGTGAACATAGGATACCATA 1396
QY 658 --HisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuAsnAspIleHisSerP 677
DB | : : : : :
1395 ATAAAATCAAGTGAACAAATAGCGACTGATAAAGTTCAAGGTGATACTATAGGA 1336
QY 677 heLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeu---HisLeuSerAsnG 696
DB | : : : : :
1335 CTATATTACCTTCAAAGAAAGCAGGCTCGTGGATTATTACAAGATAATATGGCAAAATG 1276
QY 696 lyGluSerGlyLysValGluGluGluValValGluGluMetMetMetIleLysAsnL 716
DB | : : : : :
1275 GTTAAATGGA-----GAAGATTTTGAAGTGGTTTACTA----- 1241
QY 716 ysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
DB | : : : : :
1240 -----GAATTAAGTAAGAANAATCTTCCACAAAT 1211

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RESULT 13

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US-10-793-626-4304/c
; Sequence 4304, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4304
; LENGTH: 3569
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
; US-10-793-626-4304

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Alignment Scores:
Pred. No.: 0.176 Length: 3569
Score: 121.00 Matches: 126
Percent Similarity: 34.3% Conservative: 105
Best Local Similarity: 18.7% Mismatches: 223
Query Match: 2.9% Indels: 221
DB: 8 Gaps: 27

US-10-041-018-383 (1-784) x US-10-793-626-4304 (1-3569)
QY 174 LysAsnLeuAspIleAsnLeuLeuSerLysGln----- 184
DB | : : : : :
2367 AGACAACCTTGACTCTAAACTAGCTCGAATAAGAAAGTTAAGCGTCTCTTATATAGTGTG 2308
QY 185 -----ThrAspPheSerLeuMetLeuHisLysArgGluLeuGlu----- 197
DB | : : : : :
2307 AATGACCTTAACCGAGCTTTAATGCAACACACAAAGTGAAGCGCTAGAGGAATTGGACCAA 2248
QY 198 -----GlnLysArgCysHisSerAsnGluMetAspGlyTyrLeuAla 211
DB | : : : : :
2247 TTAGGTTTTAAACTAACCAGACGTGAACGAGTATCAGATATTGAGGCGCTACTTAAT 2188
QY 212 TyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMet 231
DB | : : : : :
2187 TATATA-----GAGAAATGGACAAGC 2167
QY 232 LysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGln 251
DB | : : : : :
2166 AAAAGAGGATCT-----TTATCTTACGAT 2143
QY 252 AsnProGlyCysLeuAsnTyrIleuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro 271
DB | : : : : :
2142 ATTGATGGTATTGTTATAAAGTTAAACGATTTATCTCAACAAGA-GGAATGGG----- 2090
QY 272 ThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeu 291
DB | : : : : :
2089 -----TTATACGCAAAATCTCC-----AAGATG 2066
QY 292 Gly-IleSerHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArgCy 311
DB | : : : : :
2065 GCGGATTGCTTATAAATTTCCAGCTGAA----- 2038
QY 311 sTrpValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPheAr 331
DB | : : : : :
2037 -----GAAGTTATTACAAAATTTTGGATTGGA 2009
QY 331 gLeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnG1 351
DB | : : : : :
2008 GCTAAGTATTGGCGTACGGGTGTTGTGACACCAACTGCAATCTAGAACCTGTAAAGT 1949
QY 351 uLeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIleLeuTy 371
DB | : : : : :
1948 AGCTGGTACTACAGTTTCAAGAGCGCTCACT-----CATAATGAAGATTTTATATACA 1898
QY 371 rGlnGluAspLeuSerSerGlyLysGlnIleLeu-----LysSerAlaAspPheLeuLy 389
DB | : : : : :
1897 TGAAGAGATATACGTATCGGAGATAGTGTGTTTATTAAAAAGCGCGGACATCATCCC 1838
QY 389 sGluIleLeSerThrAspSerAsnArgLeu-----SerLysLeuIleHisLysG1 406
DB | : : : : :
1837 TGAAGTGTAAAAAGTATTTTAGATAGACGACCTAACGAATCGGAAATTTATCATATGCC 1778
QY 406 uVal-----GluAsnAlaLeuLysPheProIleAsnThrGlyLeuG1 420
DB | : : : : :
1777 AACACATTGCTCTAGTTGTGGACATGAATTAGTTCGTATTGAAGGAGAAAGTTGCTTTACG 1718
QY 420 uArgIleAsnThrArgArgAsnIleGlnLeu----- 430

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Db 2284 ACTGCAGCCATTATATTCAGATATCGTTTACCTGCTGCAACTTGGTATGAAACACAT 2343
Qy 201 ---CysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIleSerGluGlyLeuGlyAsn 219
Db 2344 GATTTATCTTACAGACATGATCCATTTATTCATCCATTTAAACCCAGCATTCACCCA 2403
Qy 220 LeuTyr-----AspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySer 235
Db 2404 TTATGGGAATCCGTTCCGAGCTGGGATTTATAAA-----ACT 2442
Qy 236 ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 2443 CTAAGTAAAGCTGTTTCAGAAATGGCGAAGATTATCTT-----CCAGGT--- 2487
Qy 256 LeuAsnTyrLeuAsnSerLeuAspLysPheGlyAsnAlaValProThrValTyrPro 275
Db 2488 -----AAATTTAAAGATGTCGTAACTACACCATTAGGA 2520
Qy 276 HisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 295
Db 2521 CATGAT-----TCAAAACAAGAAATTTCAACTGAATACGCTATTGTAA 2565
Qy 296 HisPhe---ArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrp----- 312
Db 2566 GATTGGCTTAAAGGAGAAATGAGGTGTCAGGTAAACAAATGCCTTAATTTTCTATC 2625
Qy 313 ValGluArgAsp---GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
Db 2626 GTAGAGCGAGACTATACACAAATTTACGATAAATTCGTTTACTGTTGGTCCAAAACCTAGAA 2685
Qy 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
Db 2686 AAAGGGAAATAGTGCTCATGCTGTGAGT----- 2715
Qy 352 LeuAlaLeuLysAspGluTyrAlaAlaLeuGlu-----ThrTyrHisAlaSer 367
Db 2716 TATAGGTTAGTAGAGAGACGAGAACTTAAAGTATAGTTAGTTGGAACCTTGGAAATGATGAT 2775
Qy 368 His---IleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAsp 386
Db 2776 AATACTATTTCAGTTAAATAATGATAGCCGAGAAATAGATACACGAGAGAAAGTAGCAGAT 2835
Qy 387 PheLeuLysGluIleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGlu 406
Db 2836 GTCATTTTGAATATATCTCTCTGCTCAAAACGGCAATTTATCACAAGTCATATGAAGAT 2895
Qy 407 ValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGlu-----Arg 421
Db 2896 TTAGAAAAT-----CAACAGGTATGGAACCTTAAAGATATTTCATAA 2937
Qy 422 IleAsnThrArgAsnIleGlnLeuTyrAsnValAspAsn-----ThrArgIleLeu 439
Db 2938 GAACGTGCTTCGAAAAGATATCATTTCTTAAACATTACTTCTCAACCAAGAGAGTGAT 2997
Qy 440 LysThrTyrThrHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGlu 459
Db 2998 CCAACTGCAGTATTCCTCGC-----TCTAATAAAGATGGAAGAGCGTACTCACCGTTT 3051
Qy 460 AspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeuGluArgTrpVal 479
Db 3052 ACACTAATGTTGAAGCTTTAGTGCCATTTAGAACACTAATCTGAGCGTCAAAGTTATTAT 3111
Qy 480 ValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPhe 499
Db 3112 ATAGATCATGAGGTATTCCAA---CAGTTTGGCGAAAGTTTACCGGTATAT----- 3159
Qy 500 SerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLys 519
Db 3160 -----AAACCTACTTTA---CCTCCAATGGTATTTTGGTCTCGTATAAAAAGTTAAA 3210
Qy 520 AsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyThrIleAspGlu 539
Db 3211 GGTGGACAGATACATTAGTGCTTCGATACCTTACCTCATGGA----- 3255

Qy 540 LeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCys 559
Db 3256 -----AAATGGAATATT-----CATTCAACTTAT 3279
Qy 560 SerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAsp 579
Db 3280 CAAGATAATGAACGATGTTGACGTTGTTAGAGGTGGACCGATGTTATGGATTCAAA 3339
Qy 580 GluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIle-----GlnThrTrp 597
Db 3340 GAA-----GACGCGCTGACCATGTTATTAAATGATAACGACTGG 3378
Qy 598 LeuGluLeuMetAsn 602
Db 3379 TTAGAAGTATACAC 3393
RESULT 15
US-10-793-626-3870/c
; Sequence 3870, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3870
; LENGTH: 3906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3870
Alignment Scores:
Pred. No.: 0.224 Length: 3906
Score: 120.50 Matches: 125
Percent Similarity: 36.0% Conservatives: 93
Best Local Similarity: 20.7% Mismatches: 258
Query Match: 2.9% Indels: 129
DB: 8 Gaps: 30
US-10-041-018-383 (1-784) x US-10-793-626-3870 (1-3906)
Qy 42 IleAspThrThrLysGluArgIleGlnLysGlnPheLysAsn-----ValGluIle 58
Db 2120 GTAGATAAATTAATAATCACCATTAGCTGAAATAATTAAGCATCAACATCCAGCTGATTAC 2061
Qy 59 SerValSerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLys 78
Db 2060 AATGTAACAGCTGCTCGTATGGCTGGTTCCTTCATATCCACAGTTTATAAAA---AAC 2004
Qy 79 SerProCysPheProGlu-----CysLeu 86
Db 2003 AGTCTATTATTGGTGAAGAGGCTAAAGATGAAGGTGATGATTCAAATGAAGCCATCTTA 1944
Qy 87 AsnTrpLeuIleAsnAsnGlnLeuAsn---AspGlySerTrpGlyLeuValAsnHisThr 105
Db 1943 CAAAAAGCATTGAATCAGTTAAATAAAGATACACAATTTTCGATAGAAGATCCAGAT 1884
Qy 106 HisAsnHisAsnHisPro-----LeuLeuLysAspSerLeuSerSerThrLeu 121
Db 1883 TTAAGAAAAAACCTCTCTAAACATTTTGTATGGAGATCTAAATTTAATTTCTAGTTCA 1824
Qy 122 AlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeu 141
Db 1823 GCT-----AAAGGACAAGATACTTTTATGAAGCACTTG 1791

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QY 142 SerPheIleGluSerAsnLeu---AlaSerAlaThrGluLysSerGlnProSerProIle 160
Db 1790 TTAGTGGCGGCTCTGGTTTAATGGCAGAGCCAAATGAAGATGATTAACAGAGGAAAT 1731
QY 161 GlyPheAspIlePheProGlyLeuLeuGluTyralaLysAsnLeuAspIleAsnLeu 180
Db 1730 AAATGGCGCGAGGATACAGAGGAAACTTGAATTTAGTATCACTTGATTTCAAGATG 1671
QY 181 LeuSerGlyGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArg 200
Db 1670 ACTGCGACGCCATATATTACAGATATCGTTTACCTGCTGCAACTTGGTATGAAACAT 1611
QY 201 ---CysHisSerAsnLeuMetAspGlyTyralaLysIleSerGluGlyLeuGlyAsn 219
Db 1610 GATTATCTCTACAGACATGCATCATTTATTCATCCATTAACCCAGGATGACCCA 1551
QY 220 LeuTyr-----AspTrpAsnMetValLysLysTyrglnMetLysAsnGlySer 235
Db 1550 TTATGGGAATCGGTTCCGACTGGGATATTTATAAA-----ACT 1512
QY 236 ValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCys 255
Db 1511 CTAAGTAAAGCTGTTTCAGAAATGGCGAAGATTTATCTT-----CCAGGT--- 1467
QY 256 LeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrPro 275
Db 1466 -----AAATTAAGATGTCGTAACTACACCATAGGA 1434
QY 276 HisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 295
Db 1433 CATGAT-----TCAAAACAAGAAATTTCAACTGAATACGGTATTGTAATA 1389
QY 296 HisPhe---ArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrp----- 312
Db 1388 GATTGGTCTTAAAGGAGAAATTCAGGTGTGCCAGGTAAACAACATGCTTAATTTTCTATC 1329
QY 313 ValGluArgAsp---GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
Db 1328 GTAGACGAGACTATACACAAATTTACGATAAATTCGTACTGTGGTCCAAACTAGAA 1269
QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
Db 1268 AAAAGGAAATAGGTGCTCATGTGTGAGT----- 1239
QY 352 LeuAlaLeuLysAspGluTyralaAlaLeuGlu-----ThrTyrHisAlaSer 367
Db 1238 TATAGCGTTAGTCAAGAGTACGAAGAACTTAAAGTATAGTTTGAACCTTGGAAATGATGAT 1179
QY 368 His---IleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAsp 386
Db 1178 AATACTATTTTCAGTTAAATGATAGACCGAGATAGATACGCGAGAAAGTAGCGAT 1119
QY 387 PheLeuLysGluIleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGlu 406
Db 1118 GTCATTTTGAATATATCTCTGCTCAAAACGGCAAAATTCACAAAAGTCATATGAAGAT 1059
QY 407 ValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGlu-----Arg 421
Db 1058 TTAGAAAAAT-----CAAAACAGGTATGGAACCTTAAAGATATTTCTATAA 1017
QY 422 IleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsn-----ThrArgIleLeu 439
Db 1016 GAACGTGCTTCTGAAAGATATCAITCTTAACACTTACTTCTCAACCAAGAGAGTGATT 957
QY 440 LysThrThrTyrHisSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGlu 459
Db 956 CCAACTGCAGTATTCCTCGC-----TCTAATAAGATGGAAGACGCTACTCACCGTTT 903
QY 460 AspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeuArgTrpVal 479
Db 902 ACAACTAATGTTGAACGTTTAGTCCCTTTTAGAACACTAATCGACGCTCAAGATTATTAT 843

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QY 480 ValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPhe 499
Db 842 ATAGATCATGAGGTATTCCAA---CAGTTTGGCGAAAGTTTACCGGTATAT----- 795
QY 500 SerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLys 519
Db 794 -----AAACCTACTTTA---CCTCCAATGGTATTTGGTCTCGTGATAAAAAAGTTAAA 744
QY 520 AsnGlyIleLeuThrValValAspPhePheAspIleGlyGlyThrIleAspGlu 539
Db 743 GGTGGACAAGATACATTAGTGTCTTCGATACCTTACACCTCATGGA----- 699
QY 540 LeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCys 559
Db 698 -----AAATGGAATATT-----CATTCAACTTAT 675
QY 560 SerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAsp 579
Db 674 CAAGATAATGAACGCATGTTGACGTTGTTAGAGGTGGACCACTTGTATGGATTCCAAT 615
QY 580 GluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIle-----GlnThrTrp 597
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QY 598 LeuGluLeuMetAsn 602
Db 575 TTAGAAGTATACAAAC 561

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Job time : 653.92 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 07:57:49 ; Search time 1700.42 Seconds
(without alignments)
3812.705 Million cell updates/sec

Title: US-10-041-018-383

Perfect score: 4113

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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4113	100.0	2792	7	US-10-041-018-361
2	4026	97.9	3117	7	US-10-041-018-362
3	2855.5	69.4	2594	7	US-10-041-018-368
4	2107.5	51.2	2638	7	US-10-041-018-367
5	2023.5	49.2	2658	7	US-10-041-018-378
6	2023.5	49.2	2658	7	US-10-041-018-381
7	2022.5	49.2	2506	7	US-10-041-018-377

8	1677	40.8	2554	7	US-10-425-114-3441	Sequence 3441, Ap
9	1668	40.6	2716	8	US-10-425-115-22041	Sequence 22041, A
10	1611	39.2	2730	8	US-10-425-115-22042	Sequence 22042, A
11	1607	39.1	80374	7	US-10-041-018-376	Sequence 376, App
12	1537.5	37.4	2223	6	US-10-259-194A-107	Sequence 107, App
13	1442.5	35.1	2070	7	US-10-437-963-19081	Sequence 19081, A
14	1337	32.5	2029	7	US-10-425-114-5988	Sequence 5988, Ap
15	1319	32.1	2313	7	US-10-437-963-36043	Sequence 36043, A
16	1273	31.0	2193	7	US-10-437-963-72156	Sequence 72156, A
17	1254	30.5	2086	7	US-10-425-114-17004	Sequence 17004, A
18	1247	30.3	2364	8	US-10-425-115-175619	Sequence 175619, A
19	1209	29.4	3666	7	US-10-437-963-72152	Sequence 72152, A
20	1114	27.1	2178	8	US-10-425-115-77869	Sequence 77869, A
21	1084.5	26.4	2705	5	US-10-041-007-1	Sequence 1, Appli
22	1084.5	26.4	2705	5	US-10-041-018-397	Sequence 397, App
23	1075	26.1	2388	5	US-10-041-007-36	Sequence 36, Appl
24	1075	26.1	2445	5	US-10-041-007-34	Sequence 34, Appl
25	1075	26.1	2622	5	US-10-041-007-32	Sequence 32, Appl
26	1062.5	25.8	2861	3	US-09-895-752-55	Sequence 55, Appl
27	1062.5	25.8	2861	3	US-09-887-586A-55	Sequence 55, Appl
28	1062.5	25.8	2861	3	US-09-903-012-55	Sequence 55, Appl
29	1062.5	25.8	2861	3	US-09-900-797-55	Sequence 55, Appl
30	1062.5	25.8	2861	3	US-09-893-820-55	Sequence 55, Appl
31	1062.5	25.8	2861	5	US-10-041-007-3	Sequence 3, Appli
32	1062.5	25.8	2861	7	US-10-041-018-365	Sequence 365, App
33	1054	25.6	2241	5	US-10-041-018-363	Sequence 38, Appl
34	1013.5	24.6	2700	3	US-09-895-752-43	Sequence 43, Appl
35	1013.5	24.6	2700	3	US-09-887-586A-43	Sequence 43, Appl
36	1013.5	24.6	2700	3	US-09-903-012-43	Sequence 43, Appl
37	1013.5	24.6	2700	3	US-09-900-797-43	Sequence 43, Appl
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39	1013.5	24.6	2700	7	US-10-041-018-363	Sequence 363, App
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41	965	23.5	2424	3	US-09-895-752-45	Sequence 45, Appl
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43	965	23.5	2424	3	US-09-903-012-45	Sequence 45, Appl
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ALIGNMENTS

RESULT 1
US-10-041-018-361
; Sequence 361, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; CURRENT APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent version 3.1
; SEQ ID NO 361
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: Stevia rebaudiana
US-10-041-018-361

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Best Local Similarity:	100.0%		Mismatches:	0
Query Match:	100.0%		Indels:	0
DB:	7		Gaps:	0

US-10-041-018-383 (1-784) x US-10-041-018-361 (1-2792)

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QY 21 LeuSerAlaIleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeu 40
DB 234 CTGTCAGCTATTTCATACAGCATCAACTTCACATGGTGGCAAACTAAATCCCACTAATCTG 293
QY 41 IleIleAspThrThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerVal 60
DB 294 ATCATTTGATACAAACCAAGACGGATCCAAAAACAGTTTTAAAAATGTAGAAAATTTCTGTT 353
QY 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
DB 354 TCTTCATATGACACAGCATGGGTAGCCATGGTCCCTTCTCCAACTCCACCAATCGCCT 413
QY 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
DB 414 TGTTCCTCGAGTCTCAATTTGGTTAAATTAATATCAGCTTAATGATGGTTTCATGGGCT 473
QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLeuLysAspSerLeuSerThr 120
DB 474 CTTGTTAATCACACTCATTAATCATATCAACCGGTGCTTAAAGATTTCTATCTTCAACA 533
QY 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
DB 534 TTAGCATGTATTGTTGCATTTAAAGATGGAATGTTGGGGAAGATCAAAATAAATAAAGGT 593
QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIle 160
DB 594 CTAAAGTTTATTGAGTCAAACTCTTGCTTCAGCTACTGAAAAGTCAACCATCTCCCAT 653
QY 161 GlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeu 180
DB 654 GGTTTTGACATCATATTCTCGTTGCTTGAGTATGCGAAAACTTGACATAAACCTC 713
QY 181 LeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArg 200
DB 714 CTTTCAAAACAAACAGATTTAGTTGATGCTACATAAGAGGGAATTGGAGCAAAAGAA 773
QY 201 CysHisSerAsnGluMetAspGlyTyrLeuAlaTyrIleSerGluGlyLeuGlyAsnLeu 220
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QY 221 TyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerPro 240
DB 834 TATGATTGGAATATGTTGAAGAATAATACAGATGAAAAATGGTTCTGTTTCAACTCACCA 893
QY 241 SerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsn 260
DB 894 TCAGCAACAGCTGCTCTTCAATTAATCATCAAAATCCCTGGTTGCTTTAAATTTAATAAT 953
QY 261 SerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIle 280
DB 954 TCACITTTGGACAAAGTTTGGTAATGAGTCCCAACAGTTTATCCTCATGATTTATTATC 1013
QY 281 ArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHisPheArgValGlu 300
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QY 361 LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLysGln 380

DB 1254 CTTGAAAACATATCATGCGTCACATATATATACCAAGAGGATTTATCTTCTGAAAAACAA 1313
QY 381 IleLeuLysSerAlaAspPheLeuLysGluIleIleSerThrAspSerAsnArgLeuSer 400
DB 1314 ATCTTTGAAGTCAGCTGATTTCTCAAGAGATAATATCCACTGATTCAAACAGGCTTTCT 1373
QY 401 LysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGlu 420
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DB 1434 CGCATAAACACTAGACGAAATATACAGCTTTACAAATGTAGACAAATACAGAATCTTGAA 1493
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DB 1494 ACTACATATCATCTCATCAATATTAGTAACACTGATTAACCTAAGGTGGCTGTGAAGAT 1553
QY 461 PheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeuGluArgTrpValVal 480
DB 1554 TTCTACACTGCGCAATCTATTATCGTGAAGAAATTAAGAGGTCTTGAAAGGTGGGGTGA 1613
QY 481 GluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSer 500
DB 1614 GAGATTAAGTTGGACAGCTCAAGTTTGTAGGCAAAAGACCGCTACTGTTATTCTCT 1673
QY 501 ValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsn 520
DB 1674 GTTGCTGCAACACTTTCGTCCTCCGAATTTATCAGATGCGGTATTTTCATGGGCGCAAAA 1733
QY 521 GlyIleLeuThrThrValValAspAspPhePheAspIleGlyGlyThrIleAspGluLeu 540
DB 1734 GGCATATTAACTACAGTAGTAGTCACTTTTGTGATTCGGTGGTACAAATCGATGAATTTG 1793
QY 541 ThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCysSer 560
DB 1794 ACCAACCTGATTCANGTGTTGAAAAATGGATGTAGATGTCACAGAGATTTGTTGTCA 1853
QY 561 GluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGlu 580
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QY 581 AlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeu 600
DB 1914 GCTTTTAAATGCAACGCGCGATGTAACTAGCCATGTTATTCAAACITTTGGTTGGAAC 1973
QY 601 MetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProThrLeuAsn 620
DB 1974 ATGAATAGTATGTTGAGAGAGCTATATGGACAAGAGATGCTTATGTGCCAACATTAAT 2033
QY 621 GluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIle 640
DB 2034 GAATATATGAAAAACGCTTACGTGTCATTTGATTTAGGCCGATTTGCAAGCGGCTATT 2093
QY 641 TyrPheValGlyProLysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeu 660
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QY 701 ValGluGluGluValValGluGluMetMetMetMetIleLysAsnLysArgLysGluLeu 720
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 Db 2514 GAAGAACAAAGG 2525

RESULT 2
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 ; Sequence 362, Application US/10041018
 ; Publication No. US20040072323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuda, Seiichi P.T.
 ; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
 ; FILE REFERENCE: P02080US1/10025547
 ; CURRENT APPLICATION NUMBER: US/10/041.018
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: US 60/259880
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 362
 ; LENGTH: 3117
 ; TYPE: DNA
 ; ORGANISM: Stevia rebaudiana
 US-10-041-018-362

Alignment Scores:
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 Score: 4026.00 Matches: 768
 Percent Similarity: 99.0% Conservative: 8
 Best Local Similarity: 98.0% Mismatches: 8
 Query Match: 7 Indels: 0
 DB: 7 Gaps: 0

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 Db 560 CTGTACGTATTCATACAGCATCACTTTCATCGTGGTGACAACTAATCCCACTAATCTG 619
 Qy 41 IleIleAspThrThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerVal 60
 Db 620 ATCATTTGATACCAACCAAGAACGGATCCAAAACTGTTTAAAAATGTAGAAAATTTCTGTT 679
 Qy 61 SerSerTyraAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
 Db 680 TCTTCATATGACACAGCATGGTAGCCATGGTCCCTTCTCCAAACTCACCCAAATCGCCT 739
 Qy 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
 Db 740 TGTTTCCTGAGTGTCTCAATTTGGTTAATTAATACAGCTTAATGATGTTTCATGGGT 799
 Qy 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
 Db 800 CTGTGTTAATCACACTCATATCATATCAATCACCGGTGCTTAAAGATTCCTATCTTCAACA 859
 Qy 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
 Db 860 TTAGCATGTATTGTCATTTAAAAAGATGGAATGTTGGGGAAGATCAATAAATAAAGGT 919

141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIle 160
 Db 920 CTAAGTTTTATTGAGTCAAAATCTTGCTTTCAGCAACTGACAAAGATCAACCATCTCCCAT 979
 Qy 161 GlyPheAspIleIlePheProGlyLeuLeuGluTyAlaLysAsnLeuAspIleAsnLeu 180
 Db 980 GGTTTTGATATCATATTCTCTGGTTTGGTGTGAGTATGCGAAAAAATCTTGGACATAAAGCTC 1039
 Qy 181 LeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArg 200
 Db 1040 CTTTCAAAACAAACAGATTTTAGTTTGTATGCTCATTAAGAGGGAATTTGGAGCAAAAAGA 1099
 Qy 201 CysHisSerAsnGluMetAspGlyTyAlaTyAlaTyAlaTyAlaTyAlaTyAlaTyAla 220
 Db 1100 TGCCATTTCAAATGAGATGATGATCTTGGCGGTATATCTCTGAAGGACTCGGTAAATTA 1159
 Qy 221 TyrAspTrpAsnMetValLysLysTyAlaMetLysAsnGlySerValPheAsnSerPro 240
 Db 1160 TATGATTTGGAATATGTTGAAGAAATATCATGATGAAAAATGGTTCTGTGTTTCAACTACCA 1219
 Qy 241 SerAlaThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyAlaAsn 260
 Db 1220 TCAGCAACAGCAGCTGCTTTCAATTAATCATCAAAATCCCGGTGTCTTAATATTATTAAT 1279
 Qy 261 SerLeuLeuAspLysPheGlyAsnAlaValProThrValTyProHisAspLeuPheIle 280
 Db 1280 TCACTTTTGGACAAGTTTGGTAATGCAGTCCCAACAGTTTATCTCTTGTATATATATC 1339
 Qy 281 ArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHisPheArgValGlu 300
 Db 1340 CGGCTTTCTATGTTGACACAAATGAAGATTAGGAATTTTACACCAATTTTTCAGAGTGGAA 1399
 Qy 301 IleLysAsnValLeuAspGluThrTyArgCysTrpValGluArgAspGluGlnIlePhe 320
 Db 1400 ATTAATAATGTTTTTAGATGAACATACAGATGTTGGTGGAAACAGATGACAAATATTC 1459
 Qy 321 MetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyArgVal 340
 Db 1460 ATGGATGTTGTAACATGCTTTTAGCTTTTCGCTTATTAAAGGATCCACGGTATAAAGTC 1519
 Qy 341 SerProAspProLeuAlaGluIleThrAsnGluLeuAlaLeuLysAspGluTyAlaAla 360
 Db 1520 TCCCCAGATCAATTTGGCTGAAATTTACTAATGAATTAGCTTTTCAAAAGACGAATACGAGCT 1579
 Qy 361 LeuGluThrTyHisAlaSerHisIleLeuTyGlnGluAspLeuSerSerGlyLysGln 380
 Db 1580 CTTGAACATATCATGCATCACAGATATATATACAAAGAGATTTATCTCTCGAAAAACAA 1639
 Qy 381 IleLeuLysSerAlaAspPheLeuLysGluIleIleSerThrAspSerAsnArgLeuSer 400
 Db 1640 ATCTTGAAGTCAGCTGATTTCTTCAAGGGATATTTCCACTGATTCATCAACAGGCTTTCT 1699
 Qy 401 LysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGlu 420
 Db 1700 AAATTAATTCACAAAGAGGTGGAAAAATGCTCTTAAGTTCCTCATCAATACCGGTTTGA 1759
 Qy 421 ArgIleAsnThrArgAsnIleGlnLeuTyAsnValAspAsnThrArgIleLeuLys 440
 Db 1760 CGATTAACACTAGACGAATATACAGCTTTTACAATGTAGACAAATCAAGAATTTCTGAAA 1819
 Qy 441 ThrThrTyHisSerSerAsnIleSerAsnThrAspTyAlaArgLeuAlaValGluAsp 460
 Db 1820 ACTACATATCACTCATCAATATATTAGTACACTTATTACCTTAGGTTGGCTGTTGAAGAT 1879
 Qy 461 PheTyThrCysGlnSerIleTyArgGluGluLeuLysGlyLeuGluArgTrpValVal 480
 Db 1880 TTCTACACCTGCCAACTCTATTTATCGTGAAGAAATTAAGGCTCTTGAAGGTGGTGGTA 1939
 Qy 481 GluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAlaTyCysTyTrpPheSer 500
 Db 1940 CAGAAATGAGTTGGACACGCTCAAGTTTGTAGCAAAAGACCCGCTACTGTTATTTCTCT 1999
 Qy 501 ValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsn 520

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Db      2000 GTTGTGCAACACTTCGTCCTCCGAAATATCAGATCGCGTATTTTCATGGGCCAAAAT 2059
Qy      521 GlyLeuThrValValAspPheAaspPheAaspGlyThrIleAspGluLeu 540
Db      2060 GGCATATTAACTACAGTAGTGTGATGCTTTTGTGATATCGGTGATCAATCGATGAATG 2119
Qy      541 ThrAsnLeuIleGlnCysValGluIlystrAsnValAspValAspIlyAspCysSer 560
Db      2120 ACCAACTGATTCAAATGTGTGAAAATAGAAATGTAGATGTGCACAAGGATTTGTTGTTCA 2179
Qy      561 GluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGlu 580
Db      2180 GAGCATGTTCCGATTTATTTTAGCATTAAGAATGCAATCTGTTGGATGGAGATGAA 2239
Qy      581 AlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeu 600
Db      2240 GCTTTTAAATGCAAGCGCGATGTAACTAGCCATGTTTATTCAAACTTTGGTTGGAACATA 2299
Qy      601 MetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTrpValProThrLeuAsn 620
Db      2300 ATGAATAGTATGTGTGAGAAGCTATATGGACAAGAGATGCTTATGTGCCAACATTAAT 2359
Qy      621 GluTrpMetGluAsnAlaTrpValSerPheAlaLeuGlyProIleValLysProAlaIle 640
Db      2360 GAATATATGGAACACCTTACGTGTCTATTTGATTTAGCCCGCATTTGTCGAAGCCGCTATT 2419
Qy      641 TyrPheValGlyProLysLeuSerGluGluIleValGluSerSerGluTrpHisAsnLeu 660
Db      2420 TACTTTGTGGGCCCAAAATATATCAGAGGAGATTTGTTGAAAGCTCTGAATATCATAATCTA 2479
Qy      661 PheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGlu 680
Db      2480 TTTAAAGCTAATGAGCACGCGAGGTTCGACTTCTTAAACGATATCCATAGCTTCAAGAGGGA 2539
Qy      681 PheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLys 700
Db      2540 TTTAAGGAAGGCNAATTAACCGGTAGCATTTGCATTTGAGTTAACCGGAAGAGTGGAAA 2599
Qy      701 ValGluGluGluValValGluMetMetMetMetMetMetMetMetMetMetMetMetMet 720
Db      2600 GTGGAAGAGAGAGGTTGTGAGGAGAGATGATGATGATGATGATGATGATGATGATGATG 2659
Qy      721 MetLysLeuIlePheGluGluAsnGlySerIleValProArgAlaCysLysAspAlaPhe 740
Db      2660 ATGAAATTAATTTTGAAGAAAATGCTAGCATTTGTTCTTAGAGCTTGTAAAGATGCAATT 2719
Qy      741 TrpAsnMetCysHisValLeuAsnPhePheTrpAlaAsnAspAspGlyPheThrGlyAsn 760
Db      2720 TGGACATGTGTCACGTGTGAAATTTTATTTTACGCAACGATGACGGGTTTACTGGAAAC 2779
Qy      761 ThrIleLeuAspThrValLysAspIleIleTrpAsnProLeuValLeuValAsnGluAsn 780
Db      2780 ACGATTTCTTGATGTGTGAAGGACATCAITTTACAAACCGTGTGGTCTTGTGAATGAAT 2839
Qy      781 GluGluGlnArg 784
Db      2840 GAAGAACAAGG 2851
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RESULT 3

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US-10-041-018-368
; Sequence 368, Application US/10041018
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US/10025547
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 368
; LENGTH: 2594
; TYPE: DNA
; ORGANISM: Lactuca sativa
US-10-041-018-368
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Alignment Scores:
Pred. No.:      1,7e-269      Length:      2594
Score:          2855.50      Matches:     541
Percent Similarity: 80.6%      Conservative: 102
Best Local Similarity: 67.8%      Mismatches:   116
Query Match:     69.4%      Indels:       39
DB:              7          Gaps:         6
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US-10-041-018-383 (1-784) x US-10-041-018-368 (1-2594)

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Qy      1 MetAsnLeuSerLeuCysIleAlaSerProLeuLeuThrLysSerAsn----- 16
Db      87 ATGAATATCGCACAGATCACATCATCCGCCATGCTGGTCTCTGTCACACATACCACAT 146
Qy      17 -----ArgProAlaAlaLeuSerAlaIle 24
Db      147 CGCTCATGGGTGTTAAATTTGCTGTTATGTTGCAATACAAACCCA-----TCGGTCTT 197
Qy      25 HisThrAlaSerThrSerHisGlyGlnThrAsnProThrAsnLeuIleIleAspThr 44
Db      198 CGTACAGCTTCT-TCACAAGCTGGACAAGTTAATCTCTACTGTCTGTCATGACCCCTTGATGTG 254
Qy      45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerTrpAsp 64
Db      255 ACCAAGAACGNAATCCGAAAGCTGTTCAACATGTGGAAAGTTCTGTTCTTCATATGAC 314
Qy      65 ThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db      315 ACAGCTTGGTAGCCATGCTCCTCTCCAAACTCTCCAAATCCCTTGTTCCTCGTAT 374
Qy      85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db      375 TGTCTGAAGCTGTTACTGGATAATCAGCTTGATGATGTTCAATGGGGTCTCTTT----- 428
Qy      105 ThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIle 124
Db      429 -----CCTCATCAGTCCCCATTAAATAAGATATCTCTCTTCAACATTAGCATGTGTA 482
Qy      125 ValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIle 144
Db      483 CTTCATTAAAAACGATGGAATGTTGGAAAGACCAAAATTAACAAAGTTTACATTACATT 542
Qy      145 GluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAspIle 164
Db      543 GAGTCAAATTTTGGCTTCAGTCACTCACAAAATCAAGCATCTCCATTTGGTTTGCATC 602
Qy      165 IlePheProGlyLeuLeuGluTrpAlaLysAsnLeuAspIleAsnLeuSerLysGln 184
Db      603 ATATTTCTGATGCTGTTGAGTATGCAAAAGATTTGGATATATAAACTCCCTTTAAACCAA 662
Qy      185 ThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSerAsn 204
Db      663 ACACATTTGAGTGTGATGTTACATGAGAGAAATTTGGAGCTAAGAAGATGTCAATCAAAT 722
Qy      205 GluMetAspGlyTrpLeuAlaTrpIleSerGluGlyLeuGlyAsnLeuTrpAspTrpAsn 224
Db      723 GGGAGGGAAGCATACTTGGCATATATCTCAGAAGGACTTTGGAAATTTAAATGACTGGAAC 782
Qy      225 MetValLysLysTrpGlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAla 244
Db      783 ATGGTGATGAATATCAAAATGAAGATGTTCTCTTTTCACTCACCTCAGCAACAGCT 842
Qy      245 AlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTrpLysSerLeuAsnSerLeuAsp 264
Db      843 TCTGTCTTATTATCATCAATAAATGCTGGTTGTTCTTTCATTATCTAATCTACTCTTCTGGAC 902
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Qy	55	AsnValGluIleSerValSerSerTyrAspThrAlaTrpValAlaMetValProSerPro	74
Db	228	AATGTTGAACACTTTCAAATTTCTGCATATGATATGCATGGGTGGCAATGGTCCCTTCTCCA	287
Qy	75	AsnSerProIysSerProCysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeu	94
Db	288	AACTCTCTTAATAAACCCTCTTTTCCCTGAGTGCATAAATCTGGGTATTAGTACTCAAAAC	347
Qy	95	AsnAspGlySerTrpGlyLeuValAsnHisThrHisAsnHisAsnHisProLeu--Leu	113
Db	348	CTGTATGGGTATGGGGCATACTC-----CATGACCATCAGTTGGTGATG	392
Qy	114	LysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysAspArgTrpAsnValGly	133
Db	393	AAAGCCACTCTCTTATCCACATTAGCATGTGTTCTTACTCTTAAGCGATGGGATATCGGT	452
Qy	134	GluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGlu	153
Db	453	GATGATCATATGACGAAGGCCCTTAGTATTTATCAAGTCTAATATAGCTTCAGTACTAGT	512
Qy	154	LysSerGlnProSerProIleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAla	173
Db	513	GAGAATCAACGGTCTCTCTGTGGGATTTGACATAAATTTCCGTGTATGATGTAGTATGCT	572
Qy	174	LysAsnLeuAspIleAsnLeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLys	193
Db	573	AAAGACTTGAAATTGAATCTACCTCTGGCATCAATGAATGGATGGTGTTCGTTCAAAG	632
Qy	194	ArgGluLeuGluGlnLysArgCysHisSerAsnGluMetAspGly-----TyrLeuAla	211
Db	633	AAAGAGTTGGAGCTTTAGAGCTGCTGTAGCAACTCTCGAAGGAGGAAAGCCTATTAGCG	692
Qy	212	TyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMet	231
Db	693	TATGTTTCAAGAAGAATTGGAAAATTACAGGACTGGGAAATGGTCATGCCATATCAAAAG	752
Qy	232	LysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGln	251
Db	753	AAGAACGGATCATCTGTTTAGTTCTCCATCCACCGCAGTGGCTTTATGACACAGAAAT	812
Qy	252	AsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValPro	271
Db	813	GATGATGCCTGTTTAAATTACCTTCGCTCAGTCTTACAAAAGTTTCATAGTTTCAGTTCCC	872
Qy	272	ThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeu	291
Db	873	GCAATATATCTCTGTATATATATATGCTGCTTTACACATGGTTGATAGCCTTCAAAAATG	932
Qy	292	GlyIleSerHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArgCys	311
Db	933	GGGATTGATGGCCATTTCAAGATGAGATTAGAGTGTATTAGATGAACATACAGCTGT	992
Qy	312	TrpValGluArgAspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg	331
Db	993	TGGATGCAAGGGAGGAAAAATATTCCTAGATGCTTCAACTTGTGCAATGGCCTCCGG	1052
Qy	332	LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu	351
Db	1053	ATGTTAGCTGTTGAAGGATATGATGTTTCTTCAGATCAATTGACTCAATTCTCAGAAAGT	1112
Qy	352	Leu-----AlaLeuLysAspGluTyrAlaAlaLeuGluThrTyr	364
Db	1113	CTCTTTTCAAAATGCGCTCGGAGGACATTTAAAGACTTTAGTGCTCACTAGAGTTAATT	1172
Qy	365	HisAlaSerHisIleLeuTyrGlnGluAsp-----	374
Db	1173	AAGGCTCCCGAGATTATCAATTTATCCGGATCAGTTTATTCGGAAAAATAAACTCTTGG	1232
Qy	375	-----LeuSerSerGlyLysGlnIleLeuLysSerAlaAsp	386
Db	1233	ACTAGTCGTTTCTCGAATCATGGATTATCTAGTGGT-----	1268

387	Qy	PheLeuLysGluIleLeSerThrAspSerAsnArgLeuSerLysLeuLeHisLysGlu	406
1269	Db	-----TCAGTTCACTTCGTAGAACATGAGAGACTCGTGAAACAAGAG	1310
407	Qy	ValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArg	426
1311	Db	GCAGTTAAATGCTTCGAGTTCCCTATAAATCACTCTCGAACGCTTATCAATAAGCGA	1370
427	Qy	AsnIleGlnLeuTyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSerSer	446
1371	Db	GCACCTGGAAGTTACAGTCGAGACATCTGTGAGGATTTCAAAACACACATATGCTGCTTA	1430
447	Qy	AsnIleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSer	466
1431	Db	AAATTTTGGTCATCAAGATTTCTTGGAACTTCGTGTAGAAGATTTCAATACCCCTGCAAGGC	1490
467	Qy	IleTyrArgGluGluLeuLysGlyLeuGluArgTTPValValGluAsnLysLeuAspGln	486
1491	Db	ATACATCGCAAGAACTGAAGAGCTTGAATAATGGTTCATCGAAACAATATGGACAAG	1550
487	Qy	LeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaIleThrLeuSer	506
1551	Db	TTGAATTTTGGAGACAGAACTAGCGTACTGCTATTTCTGCTGACGACCCCTAAC	1610
507	Qy	SerProGluLeuSerAspAlaArgIleSerTTPAlaLysAsnGlyIleLeuThrThrVal	526
1611	Db	TCGCCAAGACTTTGTGATGCCGCTTATCATGGCAAAAAATGGGTACTTCACAACCGTG	1670
527	Qy	ValAspAspPheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCys	546
1671	Db	GTGTGATGATTTCTTCATGTTGGAGATCTGAAGAGGAATTTGTTAAACCTTTATACAA	1730
547	Qy	ValGluLysTTPAsnValAspValAspLysAspCysCysSerGluHisValArgIleLeu	566
1731	Db	GTGGAAGTGGATGCCAGTCGGGAAACGGGTACTGTTCCAAGGAGGTTGAGATTATA	1790
567	Qy	PheLeuAlaLeuLysAspAlaIleCysTTPilleGlyAspGluAlaPheLysTTPGlnAla	586
1791	Db	TTTCTTTGCATTCATAGCACAAATTTGTGAATAGGAAAAAAATGCTTTACCTTGGCAAGGA	1850
587	Qy	ArgAspValThrSerHisValIleGlnThrTTPLeuGluLeuMetAsnSerMetLeuArg	606
1851	Db	CGACGCGTGATGAGGAATGTTATCGATAATTTGGTTCGCTTTCGAGTCAATGAGGAAG	1910
607	Qy	GluAlaIleTTPThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAla	626
1911	Db	GAAGCTGAATGGTTGAAAAATAAGGTAGTGCCATCATTCGATGATGATACATGGAAATGGC	1970
627	Qy	TyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLys	646
1971	Db	TATGTATCATTTGCTTTGGACCTATAGTCTCTCCAAACGCTCTACTTTGTTGGACCTAAG	2030
647	Qy	LeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThr	666
2031	Db	CTTCCAGAGGAAATTTGTTGAAAATGTGAAATCAAGAAGCTCTTTAAGCTGATGAGACCT	2090
667	Qy	GlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeu	686
2091	Db	TCGTGGCGCCTCTGATGATGATCTGAACCTTTGATAGAGAGTCCACGAGAGGAATTA	2150
687	Qy	AsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGluGluGluValVal	706
2151	Db	AATGCCTTGCTCTATACATGATTAGTCGCGGTGTAAGCTCCACCAAGAGGAGGCCACT	2210
707	Qy	GluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGlu	726
2211	Db	GAAGCAATGAAAGAGATGTTGTATAGCAGAGAGAGAACTGTTGAGATTAGTTTTCGAC	2270
727	Qy	GluAsnGlySerIleValProArgAlaCysLysAspAlaPheTTPAsnMetCysHisVal	746
2271	Db	GAGAAC---AGTACAATTCAGAGCTTGTGAAGATTTGTTCTGGAAAAATGACCTGTGTT	2327
747	Qy	LeuAsnPhePheTyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrVal	766

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Db 2328 GTGCATCTATTTTACAGGAAGATGATGGCTTTTACATCCCATGAGTTGATGAACCTCTGCG 2387
Qy 767 LysAspIleIleTyrAsnProLeuValLeu 776
Db 2388 AAAGCCTTATTTGAACAACCCATGGTTCTG 2417

RESULT 5
US-10-041-018-378
; Sequence 378, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 378
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Coding
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2658)
; OTHER INFORMATION: Coding
US-10-041-018-378

Alignment Scores:
Pred. No.: 1.05e-187 Length: 2658
Score: 2023.50 Matches: 393
Percent Similarity: 69.1% Conservative: 150
Best Local Similarity: 50.0% Mismatches: 212
Query Match: 49.2% Indels: 31
DB: 7 Gaps: 8

US-10-041-018-383 (1-784) x US-10-041-018-378 (1-2658)
Qy 16 AsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThrSerHisGlyGlyGlnThr 35
Db 147 TCCCGACCTACCGCGGTGGCCGCTTTTGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 206
Qy 36 AsnProThrAsnLeuIleLeuAspThr----- 44
Db 207 CTATTCCTCGAGTGGATGGGACACACAACTAAACTGGAGCTTTGGACATTTGAAGAA 266
Qy 45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerThrAsp 64
Db 267 ACAAAAGAAAGAAATTAAAGAAATTGTTTCGACAAAGTTGAACTTTTCAGTTTCTGCATATGAT 326
Qy 65 ThrAlaTyrValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db 327 ACTGCAAGGTGGCAATGGTTCCTCTCCAACTCTCTCAACCAACTCTTTTCCCGAG 386
Qy 85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db 387 TGTATAAATCGGTATAGATAGTCAACATGCTGATGGCTCATGGGCGCTACTC----- 440
Qy 105 ThrHisAsnHisAsnHisProLeuLeu---LysAspSerLeuSerSerThrLeuAlaCys 123
Db 441 -----CACAAACATCAGTTGCTGATGAAGGCCAACTCTTATCTACATTAGCATGT 491
Qy 124 IleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPhe 143
Db 492 GTTCTTACTCTTAAAGCGGTGAATATTGGGCATGATCATATGAGCAAGGCCCTTGATTTT 551
Qy 144 IleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAsp 163
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Db 552 ATCAAGCTAAATAGCTTTCAGCTACTGATGAGAACCAACGTTCTCCGGTGGGATTGAC 611
Qy 164 IleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuSerLys 183
Db 612 ATTATTTTCCCTGGCATGATTGATGATGCTTAAAGACTTGAATTTGAATTCACCTTGGCA 671
Qy 184 GlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHisSer 203
Db 672 CCGACGAAACGTGGATGCTTGGTTCCGAAAGAAAGAGTTGGAGCTGAGAAGCTGCAGAACG 731
Qy 204 AsnGluMetAspGly-----TyrLeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyr 221
Db 732 AACTCTGAAGGTGGAAGAGCCTATTTAGCGTATGTTTTCAGAGGAATTTGAAAGATTACAG 791
Qy 222 AspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSer 241
Db 792 GACTGGGATATGGTCATGCAATATCAAGGAAGAAATGGATCCTGTTTAAATTCCTCATCC 851
Qy 242 AlaThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSer 261
Db 852 ACTACGGCAGCGCTTTTATGTCATAGAAATGATGATGGCTGTTTGTATATCTTCGCTCA 911
Qy 262 LeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArg 281
Db 912 CTCTTACAAAAGTTTGCATGGCTCAGTTCACCAATATATCTCTGATATATATGCTCGA 971
Qy 282 LeuSerMetValAspThrIleGluArgLeuGlyLysSerHisHisPheArgValGluIle 301
Db 972 TTACACATGGTTGATAGCCTTCAAAATTCGGAATTCGCGCAATTTCAAAGAGGAGATT 1031
Qy 302 LysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAspGluGlnIlePheMet 321
Db 1032 AGAAGGTATTAGATGAACTTACAGTGTTCGATCGAAGGAGGAAATATATATCTTA 1091
Qy 322 AspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrGluValSer 341
Db 1092 GATGCTTCAACTTGTCAATGGCTTTCGAATGTTACGTGTTGAAGGATATGATGTTCT 1151
Qy 342 ProAspProLeuAlaGluIleThrAsnGluLeu-----AlaLeu 354
Db 1152 TCAGACCAGTTCACCTCAATTTTCAGAAAGATATCTTTCCCAATTCCTTGGAGGATATTA 1211
Qy 355 LysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAsp 374
Db 1212 AAAGACTTCGGTGGCTCGCTGGAGTTATATAGGCCCTCTCAGATTATCAGCACCCCGAT 1271
Qy 375 LeuSerSerGlyLysGlnIleLeuLys---SerAlaAspPheLeuLysGluIleLeuSer 393
Db 1272 GAATCTGTTCTCGAAATAATAAATCTTCGACTAGTCTGTTCTTCTGAAGCATGATATCT 1331
Qy 394 ThrAsp-----SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1332 AGTGATTCAGTTTGGTCTGATAGACCGGATAGTGTGTTTAAACCAAGAGGCTGTATAATGCT 1391
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1392 CTGTGATTCCTCTATTAATGCAACTCTAGAACCGCTTAATAAGTAAGGCGCAATGGAAAGT 1451
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSerSerAsnIleSerAsn 450
Db 1452 TACAGTGGAGACATCTGTAGGATTTTCAAAATCGCCATATCGCTGCTTAAATTTTGGCCAT 1511
Qy 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1512 CAAGATTTTCTGGAACCTTCGTAGAGGATTTCAATACCTTCCCTGCACCGCATTCATCTTAA 1571
Qy 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1572 GAAGTGGAGAGCTTCAAGAGATGGGTGGTTGAAACAAATTTGACGAGTGAATTTTTC 1631
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
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Db 1632 AGACTGCACCTAGGTACTCTATTTTGTCTGGGAGCGACCCCTTACTGATCCTGAACTT 1691
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspPhe 530
Db 1692 CATGATGCTCGCATAGATGGGCACAAATGGTGTCTCACCAGCGTGTGATGATTC 1751
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
Db 1752 TATGATGGTGGAGGATCTGAAGAGGAATGGATTAACCTTTATAGAAATGGTGGAAAGTGG 1811
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1812 GATCTGATGGGAAGTGGGTACTGTTCCAGGAGCTTGAGATTTGATTTCTTGCACTG 1871
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1872 CACAGCACAGTTTGTGAATAGGAAGAGAGCTTTAGTAGTGCAGGAGCGAGTGTATG 1931
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
Db 1932 AGGAATGTTATCGATGTTGGTGGCTCTGCTGAAGGTGATGAGAAGGAAGCTGAATGG 1991
Qy 611 ThrArgAspAlaTyrrValProThrLeuAsnGluTyrrMetGluAsnAlaTyrrValSerPhe 630
Db 1992 TCGACAAATAAGGTAGTGCATCAATGGGTGAATATATGGAACAGCCCATGTATCATTC 2051
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrrPheValGlyProLysLeuSerGluGlu 650
Db 2052 GCGTTGGGACCTATAATCTTCAATGCCTCTTTGTTGGACCTAAACTCTCAGAGGAA 2111
Qy 651 IleValGluSerSerGluTyrrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeu 670
Db 2112 ATGATTTGAAGCTGTGAATACCAAGAGTATATATAAGCTGATGAGCACTGCTGTCGCTT 2171
Qy 671 LeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAla 690
Db 2172 AGAATGATATTCGATCTTACCATAGAGAAATGCAAGAGGGAAGCTGAATATTCGTCT 2231
Qy 691 LeuHisLeuSerAsnGlyGluSerGlyLysValGluGluGluValValGluMetMet 710
Db 2232 CTGTGATGATTCATGCGCGTGTGAATATGTCACCAAGAGAGAGGCCATTGAACCAATAA 2291
Qy 711 MetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySer 730
Db 2292 GGGGATTTTCAGAGGGCGGATAAGAGAGCTGCTGGGGTATGTTTGCAGGAGAAC---ACT 2348
Qy 731 IleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePhe 750
Db 2349 ACAATTTCCAAGAGCTTGTAAAGGATTTGTTCTGAAATGATGTCCCATTTGTGAATCTATTT 2408
Qy 751 TyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIle 770
Db 2409 TACATGGAAGATGATGGGTACACTTCAATAGTTGATGATGACACTGTAAAAGCCATGTTT 2468
Qy 771 TyrAsnProLeuValLeu 776
Db 2469 GAACAACCACTGATCTG 2486
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RESULT 6

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US-10-041-018-381
; Sequence 381, Application US/10041018
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080051/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
```

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; SEQ ID NO 381
; LENGTH: 2658
; TYPE: DNA
; ORGANISM: Cucurbita maxima
US-10-041-018-381

Alignment Scores:
Pred. No.: 1,05e-187 Length: 2658
Score: 2023.50 Matches: 393
Percent Similarity: 69.1% Conservative: 150
Best Local Similarity: 50.0% Mismatches: 212
Query Match: 49.2% Indels: 31
DB: 7 Gaps: 8

US-10-041-018-383 (1-784) x US-10-041-018-381 (1-2658)
Qy 16 AsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThrSerHisGlyGlnThr 35
Db 147 TCCGACACCTACCGCGGTGGCCGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 206
Qy 36 AsnProThrAsnLeuIleIleAspThr----- 44
Db 207 CTATTCCCTGGAGTGGATGTGGACACAACTAAAACTGGAGCTTTGCACCTTTGAAGAA 266
Qy 45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTrpAsp 64
Db 267 ACAAAGAAAGAAATTAAGAAATTTTCGACAAAGGTGAACCTTTCAGTATTCATATGAT 326
Qy 65 ThrAlaTrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGlu 84
Db 327 ACTGATGCTGGTGGCAATGTTCTCTCCAACTCTCTCAACCAACCTCTTTTCCCGAG 386
Qy 85 CysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHis 104
Db 387 TGTATAAACTGGTATTAGATAGTCAACATGCTGATGGCTCATGGGCTCTACTC----- 440
Qy 105 ThrHisAsnHisAsnHisProLeuLeu---LysAspSerLeuSerSerThrLeuAlaCys 123
Db 441 -----CACACGATCAGTTGCTGATGAAGGCCAATCTCTTATCTACATTAGCATGT 491
Qy 124 IleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPhe 143
Db 492 GTTCTTACTCTTAAACGGTGGATATTTGGCGATGATCATATGAGCAAGCCCTTGATTTT 551
Qy 144 IleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAsp 163
Db 552 ATCAAGTCTAATAGTTCAGCTACTGATGAGAACCAACGTTCTCCGGTGGGATTTGAC 611
Qy 164 IleIlePheProGlyLeuLeuGluTyrrAlaLysAsnLeuAspIleAsnLeuSerLys 183
Db 612 ATTATTTTCCCTGGCATGATGAGTATGCTAAAGACTTGAATTTGAATCTACCTTTGGCA 671
Qy 184 GlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSer 203
Db 672 CCGACGAACCTGGATGCCCTTGGTTCCAAAGAAAGTTGGAGCTGAGAGCTGCAGAACG 731
Qy 204 AsnGluMetAspGly-----TyrLeuAlaTyrrIleSerGluGlyLeuGlyAsnLeuTyrr 221
Db 732 AACTCTGAAGGTGGAAAGCCCTATTATGCGTATGTTTTCAGAAAGGAATTCGAAAGTTACAG 791
Qy 222 AspTrpAsnMetValLysLysTyrrGlnMetLysAsnGlySerValPheAsnSerProSer 241
Db 792 GACTGGGATATGTCATGCAATATCAAGAGAAATGGATCACTGCTTTTAAATTTCTCCATCC 851
Qy 242 AlaThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTrpLeuAsnSer 261
Db 852 ACTACGGCAGCGCTTTTATGCTAGATAAGATGATGCGTGTGTTGATTATCTTCCTCA 911
Qy 262 LeuLeuAspLysPheGlyAsnAlaValProThrValTyrrProHisAspLeuPheIleArg 281
Db 912 CTCCTTACAAAAGTTTGTGCTCAGTTCCTCCCAATATATATCTCTTGTATATATATGCTCGA 971
Qy 282 LeuSerMetValAspThrIleGluArgLeuGlyIleSerHisPheArgValGluIle 301
```


Db 972 TTACACATGCTGATACGCTTCAAAATTCGGAATTCGCGCATTTCAAAGAGGAGATT 1031
Qy 302 LysAsnValLeuAspGluThrTyArgCysTrpValGluArgAspGluGlnIlePheMet 321
Db 1032 AGAAGCGTATTAGATGAACCTTACAGGTGTGTGAATGCAAGAGAGAAATATATTCTTA 1091
Qy 322 AspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyArgValSer 341
Db 1092 GATGCTTCAACTGTGCAATGCGCTTTCGAATGTACGTGTGAAGATATGATGTTCT 1151
Qy 342 ProAspProLeuAlaGluIleThrAsnGluLeu-----AlaLeu 354
Db 1152 TCAGACCAAGTGAATCAATTTTCAGAGATATCTTTCCCAATTCGCTTGGAGGATATTA 1211
Qy 355 LysAspGluThrAlaAlaLeuGluThrTyArgHisAlaSerHisIleLeuTyArgGluAsp 374
Db 1212 AAAGACTTCGCTCGCTCGAGATTATATAAGCCCTCTCAGATTATCACGCCACCCGAT 1271
Qy 375 LeuSerSerGlyLysGlnIleLeuLys---SerAlaAspPheLeuLysGluIleIleSer 393
Db 1272 GAATCTGCTCGAAATATAAATCTTGGACTAGTCTGTTCTCGAGCATGGATTATCT 1331
Qy 394 ThrAsp-----SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1332 AGTGATTACGTTGGTCTGATGAACCGATAGTGTGTGTAACACAGAGGCTGTTAATGCT 1391
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1392 CTTGAGTTCCTCCCTATATAGCACTCTAGAACCGCTTAATAAGTAAGAGGCAATGGAAGT 1451
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyArgHisSerSerAsnIleSerAsn 450
Db 1452 TACAGTGGACATTTGGAGATTTCAAAATCGCCATATGCCCTGCTTAATTTTGGCCAT 1511
Qy 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1512 CAAGATTTCTCGAACTTGCTGTAGAGATTTCAATACCTCGCAACGCAATTCATCTTAA 1571
Qy 471 GluLeuLysGlyLeuGluArgTTPValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1572 GAACCTGGAAGAGCTTCAAGATGGGTGGTGTGTAACCAAAATGACAGATTTGAAATTTTC 1631
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1632 AGACTGCACCTAGGTACTGCTATTGCTGGCGCAGCACCTTACTGATCTCTGAACTT 1691
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrValValAspAspPhe 530
Db 1692 CATGATGCTCGCATAGCATGGGCACAAATGGTGTGCTCAGCACCGTGGTGTGATGATTC 1751
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
Db 1752 TATGATGGTGGAGAGCTCTGAAGAGGAATTTGGATAACCTTATAGAAATTTGGTGAAGATGG 1811
Qy 551 AsnValAspValAspLysAspCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1812 GATCCTGATGGGAAGTGGTGTACTGTTCCAGAGCATGTGAGATTGATTTCTTGCACTG 1871
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1872 CACAGCACAGTTGTGAATAGGAAGAGAGCTTTAGTAGGCAAGGACCGACGTGTTATG 1931
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
Db 1932 AGGAATGTTATCGATGGTGGTGTCTGCTGAAGGTGATGAGAAAGCAAGTGAATGG 1991
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 1992 TCACAAATAGGTAGTGGCCATCAATGGGTGAATATATATGAAACAGCCCATGATCATTC 2051
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650

Db 2052 GCGTTGGACCTATAATCCCTTCAATGCTCTCTTTGTTGGACCTAAACTCTCAGAGAA 2111
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeu 670
Db 2112 ATGATTGGAAGCTGTGTAATACCAAGAGTTATATAAGCTGTAGGACACTGCTGGTGGCTT 2171
Qy 671 LeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAla 690
Db 2172 AAGAATGATATTTCGATCTTACGATAGAGATGCAAGAGGGAAGCTGAATATTCTGTCT 2231
Qy 691 LeuHisLeuSerAsnGlyGluSerGlyLysValGluGluValValGluGluMetMet 710
Db 2232 CTGTGATGATTGATGCGGTGTAATGTCACCAAGAGAGGAGCCATTGAAGCAATAAA 2291
Qy 711 MetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySer 730
Db 2292 GGGGATTTGAGAGGGGATAGAGAGCTCTCGGGTTAGTTTTCAGGAGAAC---ACT 2348
Qy 731 IleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePhe 750
Db 2349 ACAATTCGAAGAGCTTGTGAAGGATTTCTCTGGAATTTGATGCTCCATTGTAATCTATT 2408
Qy 751 TyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIle 770
Db 2409 TACATGGAAGATGATGGTACACTTCAATATAGGTGTGATGAACACTGTAAAAGCCATGTT 2468
Qy 771 TyrAsnProLeuValLeu 776
Db 2469 GAACAACCCATGGATCTG 2486

RESULT 7

US-10-041-018-377
; Sequence 377, Application US/10041018
; Publication No. US2004007232A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 377
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-041-018-377

Alignment Scores:
Pred. No.: 1,21e-187 Length: 2506
Score: 2022.50 Matches: 409
Percent Similarity: 68.3% Conservative: 137
Best Local Similarity: 51.2% Mismatches: 224
Query Match: 49.2% Indels: 29
DB: 7 Gaps: 11

US-10-041-018-383 (1-784) x US-10-041-018-377 (1-2506)

Qy 4 SerLeuCysIleAlaSerProLeuLeuThrLysSerAsn---ArgProAlaAlaLeuSer 22
Db 41 GCGGTTTCGGTTCCTCTGCTTCTTATGCTCTATCAACCTTCGCTCCGTTGTTGCG 100
Qy 23 AlaIleHisThrAlaSerThrSerHisGly-----GlyGlnThrAsnProThr 38
Db 101 TCTCCGATCTCAGCTACTTTGGAACGAGGATTTGGACTCAGAACTCAGACAGAGCTAAC 160
Qy 39 AsnLeuIleIleAspThrThrLysGluArgIleGlnLysGlnPheLysAsnValGluIle 58
Db 161 AATGTGAGCTTTGAGCAAAACAAAGGAGAGATTTAGGAAGATGTTGGAGAAAGTGGAGCTT 220


```
Db 1603 GTGGTGTGATGACTCTTCCTGATGTTGGTGATCAAAAGAGAATTAGAAACCTGATAGCA 1662
Qy 546 CysValGluLysTrpAsnValAspValAspLysAspCysCysSerGluHisValArgile 565
Db 1663 CTAGTTGAGAAATGGCATCGCACCATGCGAGTTGAGTTCTATTTCGGAACAGGTGAAATA 1722
Qy 566 LeuPheLeuAlaLeuLysAspAlaLeuCysTrpIleGlyAspGluAlaPheLysTrpGln 585
Db 1723 GTATTTCCTGCTATTATACAACAGTGAACCATCTTTGGAGCAATGGCTTCTCGACGACAA 1782
Qy 586 AlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeu 605
Db 1783 GCGCGTGATCTTACAAACCACTAGTAGAAATATGGCTGGATTTGTAGATCTATGATG 1842
Qy 606 ArgGluAlaIleTrpThrArgAspAlaTrpValProThrLeuAsnGluTrpMetGluAsn 625
Db 1843 GTCGAGGCAGAAATGGCAGAGATGCCAATATGTACCAACAGATTGGAAGAATACATGACAAAT 1902
Qy 626 AlaTrpValSerPheAlaLeuGlyProIleValLysProAlaIleTrpPheValGlyPro 645
Db 1903 GCTGTGTCTCATTTGCACTGGGCCCAATGTGTCTCCAGCATGTGTATTTTGTAGGGCAA 1962
Qy 646 LysLeuSerGluGluIleValGluSerSerGluTrpHisAsnLeuPheLysLeuMetSer 665
Db 1963 GAGCTATTAGACATGCTGTCAAGATGAAGAGTAGATGATAAATTATTTAGGCTAGTAGC 2022
Qy 666 ThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLys 685
Db 2023 ACTTGGCGGAGGCTCTCAATCACTACCAAAAGTTTAGAGAGGGAGGCAACAGGGAG 2082
Qy 686 LeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGluGluVal 705
Db 2083 CTGAATAGTGTCTCTACTTGTCTCCACAGTGTGTCTATGTATGCTCCATAGAAGCCGCT 2142
Qy 706 ValGluGluMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePhe 725
Db 2143 AAAAGGCCAATCAGAAAGTCCATAGACGTGCTTAGAGAGACTGTCTGAAGATGTGTCTC 2202
Qy 726 GluGluAsnGlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHis 745
Db 2203 AGGAAGAA--AGTCTGCTTCTTAGGCCATGCAAGGAGCTCTCTTGGAAGATGTGTAG 2259
Qy 746 ValLeuAsnPhePheTrpAlaAsnAspAspGlyPheThrGly--AsnThrIleLeuAsp 764
Db 2260 ATACTTCACTGTTTACTCTCAGAATGATGATTTAGCTCCCAAGGAAATGGTCACT 2319
Qy 765 ThrValLysAspIleIleTrpAsnProLeuValLeuValAsn 778
Db 2320 GCAGTGAATGCTGTTATCAACGAGGCCACTCAAAGTCCAAAAT 2361
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RESULT 9

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US-10-425-115-22041
; Sequence 22041, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22041
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120098C.1
; US-10-425-115-22041
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Alignment Scores:
Pred. No.: 9.51e-153 Length: 2716
Score: 1668.00 Matches: 351
Percent Similarity: 62.0% Conservative: 141
Best Local Similarity: 44.2% Mismatches: 260
Query Match: 40.6% Indels: 42
DB: 8 Gaps: 9
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US-10-041-018-383 (1-784) x US-10-425-115-22041 (1-2716)

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Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeuSerAlaIleHisThr 26
Db 114 CTGGTGTCCTGATGCTATCTGATTCCTTTCTCCACAGCGTATGCCAGAGCGGTG 173
Qy 27 AlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAspThrThrLys 46
Db 174 GTTGCAGAAAAC-----ACAAGCCTGCCAAACATGCATAGAAGAACTTGAG 221
Qy 47 GluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTyrAspThrAla 66
Db 222 ACTATAATAAGGAATCAGCTCCGGAAGCCCACTTGTGCCACCTTCTTCATACGACACAGCG 281
Qy 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
Db 282 TGGGTTTCTATGTCGCCAGTGGCGGGCTCTCATCAGACTCCCGCTTCCACAGTGTGT 341
Qy 87 AsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
Db 342 GAGTGGATATTGCAGAAATCAGCAGGATGATGATCTTGGGGTGTG-----AGC 389
Qy 107 AsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIleValAla 126
Db 390 CAATCTGACTCATCTCGCTCAGCAAGGATGTTCTCTATCCACGTTGGCATGTGTCTTGGC 449
Qy 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLysSerPheIleGluSer 146
Db 450 TTGAAGAGATGAATGTTGGCAGAGAGAAACATTTGGAGAGGACTGCATTTCTATCGGAGG 509
Qy 147 AsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAspIlePhe 166
Db 510 AATTTCTCTGTTGCTATGACACCAGCTTCACTTCTCTATAGTTTCAACATCACCTTT 569
Qy 167 ProGlyLeuLeuGluTrpAlaLysAsnLeuAspIleAsnLeuLeuSerLysGlnThrAsp 186
Db 570 CCTGTTTGTCTTAACTCGGCATTTGATATGGGTTTGAAGATTTCTCTGTAAAGACAACTGAT 629
Qy 187 PheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHisSerAsnGluMet 206
Db 630 GTCTGTGGCATTTCTTCCCGCGGAGAGTGAATTTGAAGAGGCTGGCTGTGATAGTTCT 689
Qy 207 AspGly-----TyrLeuAlaTrpIleSerGluGlyLeuGlyAsnLeuTrpAspTrp 223
Db 690 TTTTGAAGAAAAGCATATATATGCTTTTATCCAGAAAGGATTCGGAATATATGCTGGACTGG 749
Qy 224 AsnMetValLysLysTrpGlnMetLysAsnGlySerValPheAsnSerProSerAlaThr 243
Db 750 GATCAAGTTATGAAGTTTTCAGAGGAAGAATGGATCATTTGTCAGCAGCTCTTCCCAACT 809
Qy 244 AlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTrpLeuAsnSerLeuLeu 263
Db 810 GCTGTTGCAATTATCCAAATACACGACCAAGCCCTTCAATACCTAATTTGTTGTTGTC 869
Qy 264 AspLysPheGlyAsnAlaValProThrValTrpProHisAspLeuPheIleArgLeuSer 283
Db 870 AGTGAATTTGGCAGTGCAGTACACAGCAATGTATCTTCAATGGTATCATGTGTCAGCTTCA 929
Qy 284 MetValAspThrIleGluArgLeuGlyLysSerHisHisPheArgValGluIleLysAsn 303
Db 930 ATGGTGGAGCGCTTTGAAAAAATGGGAATTTCTCAGCGCTTTGTCAGTGAAATAGAAAGC 989
Qy 304 ValLeuAspGluThrTrpArgCysTrpValGluArgAspGluGlnIlePheMetAspVal 323
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Db 990 ATCTGACATGGCATAACAATTCCTGTTACAGAAAGATGAGAAATCATGATGCACATA 1049
QY 324 ValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrGluValSerProAsp 343
Db 1050 GCAACATGTCATGGCATTCGCTTTGAGGATGAATGTTACAAATGTTTCTTCAGAT 1109
QY 344 ProLeuAlaGluIleThrAsnGluLeuAlaLeuLysAspGluTyrAlaAlaLeuGluThr 363
Db 1110 GAGCTGCTCAGCTT-----GCTGGAGCTTCCTCACT 1139
QY 364 TyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSer----- 377
Db 1140 TTCATGATTCATACAGGATATTTAAATGATACAAAATCCCTACTGGAATTTGACAAAG 1199
QY 378 ---GlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleLeuSerThrAspSer 396
Db 1200 ACCTCAAAAGTCACCTTATCAGAAACGATCTGATCTTAGATCGCATAGGTTCTCGTCT 1259
QY 397 AsnArgLeuSerLys-----LeuIleHisLys 405
Db 1260 GGCAACTTATGAAGGATAGATGCTGTAGTAGGTGCAAAAGACTCGATTTTGGGA 1319
QY 406 GluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArg 425
Db 1320 GAGATGGAGTATGCTGTTAAATTTCCCTGTTATTCACACTGGAGCGCTTAGAACACAAG 1379
QY 426 ArgAsnIleGlnLeuTyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSer 445
Db 1380 AGAAACATCAACAATTTTGATGCTTGGGGTCTCTGATGCTA---ACAACAAAATCCTCA 1436
QY 446 SerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGln 465
Db 1437 TCTTTTCGATCATCAAGAAATTCCTAGCTTTGGCAGTCGAAGATTCAGTTTCTCTCAA 1496
QY 466 SerIleTyrArgGluGluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAsp 485
Db 1497 CGTGTTCGCGGATGAATTCGCGCATCTTGATAGTTGGGTGAAGGAGAACAAAGCTGGAC 1556
QY 486 GlnLeuLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeu 505
Db 1557 CAGCTACAATTTGCTCGCGAAGAACTGACATATTTGCTATCTGCTGCTGCTACCGTA 1616
QY 506 SerSerProGluLeuSerAspAlaArgIleSerTyrAlaLysAsnGlyIleLeuThrThr 525
Db 1617 TTTTCTCTGAATGTCTGACGCTCGCATTTTCATGGCCAAAATGGTGTCTCTCACAACT 1676
QY 526 ValValAspAspPhePheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGln 545
Db 1677 GTGGTTGATGACTTCTTCGATGTTGGTGGATCAAAAGAACATTTAGAAAACCTGATAGCA 1736
QY 546 CysValGluLysTyrAsnValAspValAspLysAspCysSerGluHisValArgIle 565
Db 1737 CTAGTTGAGAAATGGCATGCGCACCATCGCATGTTGAGTTCTATTTCGGAACAGGTGAATA 1796
QY 566 LeuPheLeuAlaLeuLysAspAlaIleCysTyrIleGlyAspGluAlaPheLysTyrGln 585
Db 1797 GTATTTTCTGCTATTATATACACAGTGAACCATCTTGGACCATGGCTTCGACAGACAA 1856
QY 586 AlaArgAspValThrSerHisValIleGlnThrTyrLeuGluLeuMetAsnSerMetLeu 605
Db 1857 GGCCGCTGATCTTACAAACACCATCTAGTAGAAATATGGCTGGATTTGTTAAGATCTATGATG 1916
QY 606 ArgGluAlaIleTyrThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsn 625
Db 1917 GTCGAGGCAGAAATGGCAGATGCCAATATGTATGTACCAACAGTTTGAAGAATAATCATGACAAAT 1976
QY 626 AlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyPro 645
Db 1977 GCTGTGTCTCATTTGCACTGGGCCCAATTTGCTCCACAGATTGATTTTGTAGGGCAA 2036
QY 646 LysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSer 665
Db 2037 GAGCTATTAGAGCATGCTGTCAAAGATGAAGAGTACGATAAATATTATTAGGCTAGTGAGC 2096
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```
QY 666 ThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLys 685
Db 2097 ACTTGGGGAGGGCTCTCTAATGACTACCAAAAGTTTAGAGAGGAGCAACACCGGGAAG 2156
QY 686 LeuAsnAlaValAlaLeuHisLeuSerAsnGlyLysSerGlyLysValGluGluVal 705
Db 2157 CTGAATAGTGTCTCTCTACTTGTGCTCCACAGTGGTGTCTATGTCTCATAGAAGCGCT 2216
QY 706 ValGluGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePhe 725
Db 2217 AAAAGGCAATGCAGAAAGTCCATAGACGTCTTAGGAGACACTTGTAAAGATTGGTCTC 2276
QY 726 GluGluAsnGlySerIleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHis 745
Db 2277 AGGAAGAA---AGTCTGTCTTAGCCCATGCAAGAGCTCTTCTGGAAGATGTGTAAG 2333
QY 746 ValLeuAsnPhePheTyrAlaAsnAspAspGlyPheThrGly---AsnThrIleLeuAsp 764
Db 2334 ATACTTCACCTGTTTACTCTCAGATGATGGATTTAGCTCCCAAGAGAAATGGTCAGT 2393
QY 765 ThrValLysAspIleIleTyrAsnProLeuValLeuValAsn 778
Db 2394 GCAGTGAATGCTCTGTTATCAACGAGCCACTCAAAAGTCCAAAAT 2435
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RESULT 10

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US-10-425-115-22042
; Sequence 22042, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22042
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_120099C.1
US-10-425-115-22042
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Alignment Scores:
Pred. No.: 3 84e-147 Length: 2730
Score: 1611.00 Matches: 345
Percent Similarity: 62.4% Conservative: 143
Best Local Similarity: 44.1% Mismatches: 249
Query Match: 39.2% Indels: 46
DB: 8 Gaps: 10
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US-10-041-018-383 (1-784) x US-10-425-115-22042 (1-2730)

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QY 35 ThrAsnProThrAsnLeuIleAspThrThrLysGluArgIleGlnLysGlnPheLys 54
Db 290 ACAAGCCTGCAAAACATCGATAGGAAGATCTTGAGACTATAATAAGGAATCAGTCCGG 349
QY 55 AsnValGluIleSerValSerSerTyrAspThrAlaTyrValAlaMetValProSerPro 74
Db 350 AAGCCCAAGTGGCACCTCTTCTCATACGACACAGCGTGGGTTTCTATGGTGCCAGTCCGG 409
QY 75 AsnSerProLysSerProCysPheProGluCysLeuAsnTyrPheLeuAsnAsnGlnLeu 94
Db 410 GGCTCTCATCAGACTCCCGCTCCACAGTGTGTGAGTGGGATCTGCGACAGACAGCAG 469
QY 95 AsnAsp-GlySerTyrPheValAsnHisThrHisAsnHisAsnHisProLeuLeu 114
Db 470 GATGATGGGATCTTGGGGTGTG-----AGCCAATCTGACTCATCGGTGAGCAA 517
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QY	114	sApSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGI	134
DB	518	GGATGTTCTCTATCCACGTTGGCATGTGTTCTCGCTTGAAGAGATGGAATGTTGGCAG	577
QY	134	uApGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLys	154
DB	578	AGAAACATTGTGAGAGGATCGATTTCATCGGAGGAATTTCTCTGTCTCTATGGAACA	637
QY	154	sSerGlnProSerProIleGlyPheAspIleIle-PheProGlyLeuLeuGluLys- Ala	173
DB	638	GCAGTTTCACCTTCCTATAGTTTCACTTCACCCCTTCTCTGGTTGCTTAGCCTCGGCA	697
QY	174	LysAsnLeuAspIleAsnLeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLys	193
DB	698	TTTGATATGGTTTAGAAATTTCCCTGTAAGACAAACTGATCTCTGTGGCATTTCTCACCGC	757
QY	194	ArgGluLeuGlnLynAsArgCysHisSerAsnGluMetAspGly-----TyrLeu	210
DB	758	CGGAGATGGAATTGAAGAGCGTGGCTGCGATGATGTTCTTTGGAAGAAAGCATATATG	817
QY	211	AlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGln	230
DB	818	GCTTTATCCAGAGGATTCGGAATATATGCTGGACTGGGATCAAGTTATGAAGTTTCAG	877
QY	231	MetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIleAsnHis	250
DB	878	AGGAAGAATCGATCATGTTCAGCACTTCCTCCACAACTGCTGTGCATTAATCCACAAA	937
QY	251	GlnAsnProGlyCysLeuAsnTyrLeuAsnSerIleLeuAsnLysPheGlyAsnAlaVal	270
DB	938	TACAACGACCACGCCCTTCATACTAAATTTGCTGTGATGAATTTGGCGATGTCAGTA	997
QY	271	ProThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIleGluArg	290
DB	998	CCAGCAATGATCTTCAATGGTACATGTGTCACTTTCAGTTTCAATGGTGGACGCGTTGAAA	1057
QY	291	LeuGlyIleSerHisHisPheArgValGluIleLysAsnValLeuAspGluThrTyrArg	310
DB	1058	ATGGGAATTTCTCAGCGCTTTGTGAGTGAATATGAAGCATCTCTGGACATGGCATACAAT	1117
QY	311	CysTrpValGluArgaspGluGlnIlePheMetAspValValThrCysAlaLeuAlaPhe	330
DB	1118	TGCTGGTTACAAAAGATGAGGAATCATGATGACATACCAACATGTGCATGGCCATTT	1177
QY	331	ArgLeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsn	350
DB	1178	CGCCTTTGAGGATGAATGTTACAATGTTTCTCTCAGATGAGCTGTCTCAGTTGTGGA	1237
QY	351	GluLeuAla-----LeuLysAspGluTyrAlaAlaLeuGlu	362
DB	1238	GCTTCCACTTTCCATGATTCCTACAGGATATTTAAATGATACAAAATCCCTACTGGAA	1297
QY	363	ThrTyrHisAlaSerHisIle--LeuTyrGlnGluAspLeuSerSerGlyLysGlnIle	381
DB	1298	TTGTACAAGACCTCAAAAGTCACCTTATCAGAAACCGATCTGATCTTAGATCGCATAGGT	1357
QY	382	LeuLysSerAlaAspPheLeuLys-----	389
DB	1358	TCCTGGTCTGGCACTTATTGGAAGATAAGATGCTAGTAGGGGTGCAAAAAGACTCG	1417
QY	390	-----GluIleIleSerThr-AspSerAsn-----ArgLeuSerLysLeuIle	403
DB	1418	ATTTTGTGAGAGGTGCTGCAACAAAATTTAAATTTCTCATTTTCCCTCGGAGGTTCCAGT	1477
QY	403	eHisLys-----GluValGluAsnAlaLeuLysPheProIleAsnThrGln	418
DB	1478	TTATGCTGTGTTTGTGATTTTCAGATGGAGATGTCGTGTTAAATTTTCCCTGTATTCCAC	1537
QY	418	yLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsnThrArgIle	438
DB	1538	ACTGGACGCTCTAGAAACAAGAGAAACATCGAACTTTGATGCTTGGGGTCTCTGAT	1597

Qy	438	eLeuYgThrThrThyHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaVala	458
Db	1598	GCTA--ACACAAAAAACCCTCATCTTTTTCGTATCAATCAAGAAATCTTACGCTTTGGCAGT	1654
Qy	458	lGluAspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLeuYsglyLeuGluArgTr	478
Db	1655	CGAAGATTTTCAGTTTCTCTCAACGTTGTACCGGGATGAATTCGGCATCTTGTATAGTTG	1714
Qy	478	pValValGluAsnLysLeuAspGlnLeuYsPheAlaArgGlnLysThrAlaTyrCysTy	498
Db	1715	GGTGAAGGAGAAACAAGCTGACACAGCTACAAATTTGTCTGGCAGAAAATGACATATTGCTA	1774
Qy	498	rPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAl	518
Db	1775	TCTGTCTGCTGCTACCGTATTTTCTCTGAATGTCTGAGCTCGCAATTTTCATGCGG	1834
Qy	518	AlaYAsnGlyIleLeuThrThrValValAspAspPheAspIleGlyThrIleAs	538
Db	1835	CAAAAAATGGTGTCTCAACAACCTGGTGTGATGACTTCTTCGATGTGTGGTGAATCAAAAGA	1894
Qy	538	pGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCy	558
Db	1895	AGAATTAGAAAACCTGTATGACCTAGTGTGAGAAATGGCATGCGCACCAATCGAGTTGAGTT	1954
Qy	558	sCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGl	578
Db	1955	CTATTTCGGAACAGGTGAAATAGTATTTTCTGCTATTTATCAACAGTGAACCATCTTGG	2014
Qy	578	YAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLe	598
Db	2015	AGCAATGGCTTCTGCAGCACAAAGCCGTGATCTTCAAAACACCTAGTAGAAAATATGGCT	2074
Qy	598	uGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProTh	618
Db	2075	GGATTTGTTAAGATCTATGATGTTGTGAGGAGCAATGGCAGAGATGCCAATATGTACCCAC	2134
Qy	618	rLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysPr	638
Db	2135	AGTTGAGAAATACATGACAAATGCTGTTGTCATTTGTCATGCGGCCCAATTTGTGCTCCC	2194
Qy	638	oAlaIleTyrPheValGlyProLysLeuSerGluGluIleValIleGluSerSerGluTyrHi	658
Db	2195	AGCAATGTATTTGTAGGGCAAGAGCTATTAGAGCATGCTGTCAAAGATGAAGAGTACGA	2254
Qy	658	sAsnLeuPheLysLeuMetSerThrGlnGlyArgGluLeuAsnAspIleHisSerPheLy	678
Db	2255	TAAATTTATTAGGTAGTGAAGTCTCGGGAGGCTCTCAATGACTACCAAGTTTAGA	2314
Qy	678	sArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlnGluSe	698
Db	2315	GAGGCAAGGCAACCAAGGGGAAGCTGAAATAGTGTGTTCTCTACTTGTGTCACACAGTGTGG	2374
Qy	698	rGlyLysValGluGluValValGluGluMetMetMetMetIleLysAsnLysArgLy	718
Db	2375	TTCTATGTCCATAGAAGCCGCTAAAAGGCAATGACAGAGTCCATAGACGTGCTAGGAG	2434
Qy	718	sGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProArgAlaCysLysAs	738
Db	2435	AGACTTGTGAAGTTGGTTCTCAGGAAGAA--AGTGCTGTTCTTAGGCCATGCAAGGA	2491
Qy	738	pAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAspGlyPheTh	758
Db	2492	GCTCTTCTGGGAAGATGTGTAAAGATACCTACCTGTTTCTCTCAGAAATGATGGATTAG	2551
Qy	758	rGly--AsnThrIleLeuAspThrValLysAspIleIleTyrAsnProLeuValLeuVa	777
Db	2552	CTCCCCAAAGAAATGTCAGTCAGTGAATGCTGTTATCAACGAGGCATCTCAAAGTCCA	2611
Qy	777	lAsn 778	
Db	2612	AAAT 2615	

RESULT 11


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QY 439 uLysThrThrTyr----- 443
Db 45199 AAAAAACCTCATATCGGTAAATTCCTCTTCTTCCCTTTAGCGTGTGTGCGCATATGTTT 45140
QY 444 -----HisSer-Ser----- 446
Db 45139 TGGCAGCCAGCTTCCATTAAACGCAATCTAATCAGGGCATTCATCTCTCATCTTGT 45080
QY 447 -----AsnIleSerAsnThrAspTyrIleuArgLeuAlaValG 459
Db 45079 TTCTTCTGTGTCTAGTTTGGCAATATTTGGACCTCTGATATCTCTGAAGTTAGCTGTGG 45020
QY 459 LuAspPheTyrThrCysGlnSerIleTyrArgGluLeuLysGlyLeuGlu----- 476
Db 45019 ATGACTTCAATTTTGCAGCTCCATACACCGTGAAGAAATGGAACGCTTGTAGTGTGG 44960
QY 476 ----- 476
Db 44959 CTCCAGCTAAGCTTTTTCATTATTATTCAGCCTTCTTGCATAAGCTAATTAGTTTACTTAA 44900
QY 476 ----- 476
Db 44899 TATATAACACACACTTGAACGAGTTTCAGTTTATAAATTCAGGTGTGACTTCTATTGTT 44840
QY 477 -----ArgTrpValValGluAsnLysL 484
Db 44839 ATGTAGTCACAATTCAGCAATGCTGCTCACCACCTTGCAGGTGGATTTGGGAGATAGAT 44780
QY 484 euAspGlnLeuLysPheAlaAArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaT 504
Db 44779 TCAGGAACCTGAATTTTGCAGACAGAGCTGGCTTACTGTATTCTCTGGGGCTGCAA 44720
QY 504 hrLeuSerSerProGluLeuSerAspAlaAArgIleSerTrpAlaLysAsnGlyLeuT 524
Db 44719 CTTTATTTTCTCTGAACTATCTGATGCTCGTATATCGTGGGCGCAAGGTGGAGTACTTA 44660
QY 524 hrThrValValAspAspPheAspIleGlyThrIleAspGluLeuThrAsnLeuI 544
Db 44659 CAACGGTTGTAGCAGCTTCTTTGTATGTTGGAGGGTCCAAAGAAGAACCTGGAACCTCA 44600
QY 544 leGlnCysValGluLysTrpAsnValAsp----- 553
Db 44599 TACACTTGTGCGAAGAATAT- --GTTGATTTGGCTCTTCTGAGCTTCTCTCTGCT 44543
QY 554 -----V 554
Db 44542 TGTTCCTCGTAAAGCATATCGTTCTTCGCTTACAAATTTTCAGGTGGGATTTGAACGG 44483
QY 554 alAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaI 574
Db 44482 TGTT-CTTGAGTACAGCTCAGAACATGTTTGAGATCATATTTCTCAGTTCTTAAGGGACCCA 44424
QY 574 leCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaAArgAspValThrSerHisValI 594
Db 44423 TTCTCGAAACAGGAGCAAGCAATTCACCTATCAGGACGCAATGTGCACACCACTTG 44364
QY 594 leGln----- 595
Db 44363 TGAATAATGTTAAGTATCAATCATCCACAAATTAATTCTCTGTTATCATAGCCCTAAC 44304
QY 596 -----Thr-TrpLeuGluLeuMetAsn 602
Db 44303 AACTCATCTGACCATACTTCATTGGTGCATATCTTACGACGTGGTGGATCTGCTCAAG 44244
QY 603 SerMetLeuArgGluAlaIleTrpTrpArgAspAlaTyrValProThrLeuAsnGluTyr 622
Db 44243 TCTATGTTGAGAGAGCCAGGTGCTCCAGTGACAGTCAACCAAGCTTGGAGGATTAAC 44184
QY 623 MetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPhe 642
Db 44183 ATGGAATAATGCGTACATATCATTTGATTTAGGACCAATTTGCTCCAGCTACCTATCTG 44124
QY 643 valGlyProLysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLys 662
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Db 44123 ATCGGACCTCCACTTCCAGAGAGACAGTCGATACCCACCAATATAATCAGCTCTACAG 44064
QY 663 LeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPhe----- 677
Db 44063 CTCGTGAGCACTATGGGTGCTTCTTAAATGACATACAAGG-TTTTAAAGGTAAGACTCTT 44005
QY 677 ----- 677
Db 44004 CTTAAATAATCTCAAACTTTTACTAAACTGTACAGTTGAAAGATGGCAAGAGCCCTAAA 43945
QY 677 ----- 677
Db 43944 TCCAACAAATAATCGTAAATTAACAACTCTGCTCATAGATTTCGGATTATATATCCCT 43885
QY 678 -----LysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHis 692
Db 43884 TTTGATGTTTTTTTTCAGAGAGAGAAAGCGCGGAAGGAGCTGAATCGCGTTTTCATTGCAC 43825
QY 693 LeuSerAsnGlyLysSerGlyLysValGluGluValValGluGluMetMetMet 712
Db 43824 ATGAACACGAGAGAGACAATCGCAGCAAGAAAGTGTATAGAAATCGATGAAGGTTTA 43765
QY 713 IleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySerIleVal 732
Db 43764 GCAGAGAAAGAGGAGAAATTCGATAGCTAGTTTTCGAGAGAGAAAGAGTGTGGTT 43705
QY 733 ProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAla 752
Db 43704 CCAAGGGAATGCAAGAGCGTTCTTGAAATGAGCAAGTGTGAACTTATTATACAGG 43645
QY 753 AsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIleTyrAsn 772
Db 43644 AAGGACGATGGATTCCACATCAATCATCATGATGCTGTTGTTAAATCATGATCTACGAG 43585
QY 773 ProLeuValLeuAsnGluAsn 780
Db 43584 CCTGTAGCTTACAGAGAAATCT 43561
RESULT 12
US-10-259-194A-107
; Sequence 107, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassseman, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 107
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-194A-107
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QY 490 AlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGlu 509
 Db 1192 GCACGGCAGAGTTGGACTACTTCTATTTCTGCTGCTGCTACCACTTTTCACTCTGAA 1251
 QY 510 LeuSerAspAlaAlaArgLysThrAlaLysAsnGlyLysLeuThrValValAspAsp 529
 Db 1252 CTGTCAGATGTTCCGCAATTTTGTGGGCCAAATAATGGCGTGTCTGACACGGTCTGCGACGAC 1311
 QY 530 PhePheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLys 549
 Db 1312 TTCTTCAGCTGGAGATCAAAAGAGAAAGTGAATCTGTCGATTAATGTTGAGAAG 1371
 QY 550 TrpAsnValAspValAspLysAspCysSerGluHisValArgIleLeuPheLeuAla 569
 Db 1372 TGGGACAGAAGTACAAAACCTGAGTACTCTCTGAAACAGTAGAGATTGTTCTCTGCA 1431
 QY 570 LeuLysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspVal 589
 Db 1432 ATTTATCTTCAACTAACCCAGCTTGGATCAATGGCCTCTGTAGTACAAGCCCGTGTATC 1491
 QY 590 ThrSerHis-ValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAla1 609
 Db 1492 ACCACACACCTTGTAGAATATGGCAAGATTTGCTGAGTCTATGATGACAGAGTAGA 1551
 QY 609 eTrpThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSe 629
 Db 1552 GTGGAGCAGAGCGCGTATGTGCCAACAGCAGAGGAATACATGGAATAATGTCAGTTGTGAC 1611
 QY 629 rPheAlaLeuGlyProIleValLysProAla-IleTyrPheVal-GlyProLysLeuSer 648
 Db 1612 ATTTCAGCTGGGACCGGTTGTGCTCCAGCAGCTGTATCTTGTGGGACCAAGATGCCT 1671
 QY 649 GluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThrGlnGly 668
 Db 1672 GATTTCTTATAGAACCAAGATGCAGCGAGTTGTTCGGTATAGCAATGTGCG 1731
 QY 669 ArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAla 688
 Db 1732 CGTCTCTGATGATCTCCATCTACAGAGAGAGGCGCAGCGCAAGCTGGAACAGC 1791
 QY 689 ValAlaLeuHisLeuSerAsnGlyGluSerGlyLysValGlu---GluGluValValGlu 707
 Db 1792 GTCTCTCTG---CTTGCCCTCCACAGCTGGAGGCTCTGTCTCCATGGAAGAGGCTGTGAAG 1848
 QY 708 GluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGlu 727
 Db 1849 CAGATTTCAGAGCCCATCAGAGAAATGCAGAGAGAGTTGCTGAAGCTGTGTCGCACAGA 1908
 QY 728 AsnGlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeu 747
 Db 1909 GGAGGCGCC---GTTCCAGGCCATGCAGGAGAGCTGTTCTGGAGCATGTGCAAGGTCTGC 1965
 QY 748 AsnPhePheTyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLys 767
 Db 1966 CACTTCTTCTACTCCGCGCGCAGCGGTTTCAGCTCCGCGACGCGGCGCGCGGTG 2025
 QY 768 Asp---IleIleTyrAsnProLeuValLeu 776
 Db 2026 GACGCGGTGATCCAGCGCGCTGAATCTG 2055

RESULT 14

US-10-425-114-5988
 ; Sequence 5988, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 5988
 ; LENGTH: 2029
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700550363_FLI
 ; US-10-425-114-5988

Alignment Scores: 2.07e-120 Length: 2029
 Pred. No.: 1337.00 Matches: 280
 Score: 62.6% Conservative: 116
 Percent Similarity: 44.2% Mismatches: 198
 Best Local Similarity: 32.5% Indels: 39
 Query Match: 7 Gaps: 7
 DB:

US-10-041-018-383 (1-784) x US-10-425-114-5988 (1-2029)
 QY 183 LysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHis 202
 Db 24 AGACAACTGATGTCTGTGGCATTTCTTACCGCGGAGATGGAATTTGAAAAGGCTGGCT 83
 QY 203 SerAsnGluMetAspGly-----TyrLeuAlaTyrIleSerGluGlyLeuGlyAsn 219
 Db 84 GTGGATAGTCTTTTGGAGAAAGCATATATGGCTTTTATCCAGAAAGGATTCGGAAT 143
 QY 220 LeuTyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSer 239
 Db 144 ATGCTGGAGTGGATCAAGTTATGAAGTTTCAGAGGAGAAATGATCATTTGTTTCAGCACT 203
 QY 240 ProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeu 259
 Db 204 CTTTCACAACTGCTGTTCATTTAATCCACAAATACACGACCAAGCCTTCAATACCTA 263
 QY 260 AsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPhe 279
 Db 264 AATTGCTTGTGATGAAATTTGGCAGTGCAGTACCAAGCAATGATCTTCAATGGTACAT 323
 QY 280 IleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisPheArgVal 299
 Db 324 TGTACGCTTCAATGTGTGGCGCTTTGAAAAATGGGAATTTCTCAGCGCTTTGTTCAGT 383
 QY 300 GluIleLysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAspGluGlnIle 319
 Db 384 GAAATAGAAAGCATCTCGACATGCGATACAATTGCTGTGTTACAGAAAGATGAGAAATC 443
 QY 320 PheMetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrGlu 339
 Db 444 ATGATGGATAGCAACATGTGCAATGGCATTTTCGCTTTTGGAGATGAATGGTTACAAT 503
 QY 340 ValSerProAspProLeuAlaGluIleThrAsnGluLeuAla----- 353
 Db 504 GTTTCCTCAGATGAGCTGTCTCAGCTGTGGAGCTTCCACTTCCATGATTCACATAA 563
 QY 354 -----LeuLysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIle---Leu 370
 Db 564 GGATATTTAAATGATACAAAATCCCTACTGGAATTGTACAAAGACCTCAAAAGTCACCTTA 623
 QY 371 TyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSerAlaAspPheLeuLysGlu 390
 Db 624 TCAGAAACGATCTGATCTTAGATCGCATAGGTTCTCTGGTCTCGCAACTTATTATTGAAGAT 683
 QY 391 IleIle-SerThrAspSerAsnArgLeuSerLysLeuIleHisLys----- 405
 Db 684 AGATGTGCTGTAGTAGGTGCAAAAGACTCGATTTTGGAGAGGTGTCGCAAAAAA 743
 QY 406 -----GluVal 407
 Db 744 TTTAAATTTCTCAATTTTTCACCTGGAGGTTTTCAGTTTATGTCTGTGTTTGTGATTTCAGAT 803

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QY 407 lgluAenAlaLeuLysPheProIleAsnThrGlyLeuGluAArgIleAsnThrArgArgAs 427
Db 804 GGAGTATGCTGTTAAATTTTCCCTTTGATTTCCACACTGGGAGCGTCTAGAACACAAAGAGAA 863

QY 427 nleGlnLeuTyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAs 447
Db 864 CATCGAATCATTTTGATGCTTGGGGTCTCTGATGCTA---ACAACAAATCCTCATCTTT 920

QY 447 nleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerI 467
Db 921 TCGTATCAATCAAGAAATTCCTAGCTTTGGCAGTCGAAGATTTTCAGTTTCTCTCAACGCTG 980

QY 467 eTyrArgGluGluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLe 487
Db 981 TTACCGGGATGAATTCGGCATCTTGATAGTTGGGTGAAGGAGAAACAAGCTGGACGAGCT 1040

QY 487 uLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSe 507
Db 1041 ACATTTGCTCGCGAAGAACTGACATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100

QY 507 rProGluLeuSerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValVa 527
Db 1101 TTCTGAATTTCTGACGCTCGCATTTTCATGGCGCAAAATGCTGCTCCTCACAACTGTGCT 1160

QY 527 lAspAspPheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysVa 547
Db 1161 TGAATGACTTCTTCGATTTGGTGGATCAAAAGAAATTTAGAAACCTGATAGCACTAGT 1220

QY 547 lGluLysTrpAsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPh 567
Db 1221 TGAGAAATGGCATGGCCACCATGTCAGTTGAGTTCTTATTCGGAAACAGGTGAAATAGTATT 1280

QY 567 eLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaAr 587
Db 1281 TTCTGCTATTTATACACAGTGAACCATCTTCGAGCAATGGCTTCGACGACACAGGCCG 1340

QY 587 gAspValThrSerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGl 607
Db 1341 TGATCTTCAAAACCACTAGTAGAAATATGGTGGATTTGTTGAAGATCTATGATGTCGA 1400

QY 607 uAlaIleTrpThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTy 627
Db 1401 GGCAGAAATGGCAGATGCCAATATGTACCAAGTTGAAGATATCATGACAAATGCTGT 1460

QY 627 rValSerPheAlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLe 647
Db 1461 TGCTCTCATTTGCACTGGGCCCAATTTGCTGCCAGCATTTGATTTTGTAGGCAAGAGCT 1520

QY 647 uSerGluGluIleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThrGl 667
Db 1521 ATTAGAGCATGCTGTCAAGATGAAGATGACGATACATAAAATTTATTTAGCTAGTGAGCACTG 1580

QY 667 nGlyArgLeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAs 687
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QY 707 uGluMetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGl 727
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RESULT 15
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; Sequence 36043, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 36043
; LENGTH: 2313
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39906C.1
US-10-437-963-36043

Alignment Scores:
Pred. No.: 1.49e-118 Length: 2313
Score: 1319.00 Matches: 288
Percent Similarity: 56.9% Conservative: 146
Best Local Similarity: 37.7% Mismatches: 223
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DB: 7 Gaps: 16

US-10-041-018-383 (1-784) x US-10-437-963-36043 (1-2313)

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QY 72 ProSerProAsnSerPro-----LysSerProCysPheProGluCysLeuAsnTrpLeu 89
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QY 90 lLeAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHisAsnHisAsn 109
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Db 484 TCATCAGCCAGCAAGATATTTCTCTCATCTTTGGCATGTATTATTGCACCTTGAGAAA 543

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Db 544 TGGAAATGTCGGTTCGAGCAAAATAGGAGAGGATTTACATTTTATCCAAAGAAATTTCTCC 603

QY 150 SerAlaThrGluLysSerGlnProSerProIleGlyPheAspIlePheProGlyLeu 169
Db 604 ATTGTTATTGATGACAGATTGCTGACCTTAGGCTTCACTTCACTTCCATTCCTCGTATG 663

QY 170 LeuGluTyrAlaLysAsnLeuAspIleAsnLeuLeuSerLysGlnThrAspPheSerLeu 189
Db 664 GTTAACCTTGCCATTAAGATGGGTTTGGAAATTTCTGCCAGTGAAATAGTATTGATCAG 723
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 06:52:12 ; Search time 383.242 Seconds
(without alignments)
3636.365 Million cell updates/sec

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
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- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2023.5	49.2	2658	3	US-08-727-308-3
3	1523	37.0	2403	3	US-09-614-912-23
4	1084.5	26.4	2705	3	US-10-041-007-1
5	1075	26.1	2388	3	US-10-041-007-36
6	1075	26.1	2445	3	US-10-041-007-34
7	1075	26.1	2622	3	US-10-041-007-32
8	1062.5	25.8	2861	3	US-09-398-395A-55
9	1062.5	25.8	2861	3	US-09-887-586A-55

Sequence 55, Appl
Sequence 55, Appl
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Sequence 55, Appl
Sequence 3, Appl
Sequence 38, Appl
Sequence 1, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 43, Appl
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Sequence 45, Appl
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Sequence 45, Appl
Sequence 45, Appl
Sequence 14, Appl
Sequence 39, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-727-308-2
; Sequence 2, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850


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Db 1992 TCACAAATAAGCTAGTGCATCAATGGGTGAATATATGTAACAAGCCCATGATCATTC 2051
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Db 2052 GCCTGGGACCTAATAATCTTCAATGCTCTCTTTGTTGGACCTAAACTCTCAGAGGAA 2111
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeu 670
Db 2112 ATGATTGGAAGCTGTGAATACCAAGAGTATATATAGCTGATGAGCACTGCTGCTGCCCTT 2171
Qy 671 LeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAla 690
Db 2172 AAGAATGATATTGATCTTACGATAGAGTAAAGAGGAGGAAAGCTGAATATTCTGTCT 2231
Qy 691 LeuHisLeuSerAsnGlyGluSerGlyLysValGluGluValValGluGluMetMet 710
Db 2232 CTGTGATGATTGATGGCGTGTGAATGTCAACAAAGAGAGGAGCCATTGAAGCAATAA 2291
Qy 711 MetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySer 730
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Qy 751 TyrAlaAsnAspAspGlyPheThrGlyAsnThrIleLeuAspThrValLysAspIleIle 770
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Qy 771 TyrAsnProLeuValLeu 776
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RESULT 2
US-08-727-308-3
; Sequence 3, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-727-308-3

Alignment Scores:
Pred. No.: 4,61e-220 Length: 2658
Score: 2023.50 Matches: 393
Percent Similarity: 69.1% Conservative: 150
Best Local Similarity: 50.0% Mismatches: 212
Query Match: 49.2% Indels: 31
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Qy 36 AsnProThrAsnLeuIleIleAspThr----- 44
Db 207 CTATTCCTCCGAGTGGATGTGGACACACAACTAAACTGGAGCTTTGCATTTTGAAGAA 266
Qy 45 ThrLysGluArgIleGlnLysGlnPheLysAsnValGluIleSerValSerSerTyrAsp 64
Db 267 ACNAAAGAAGAATTAAGAAATTTGTCGACAGGTTGAAGTTTCACTTTCTGATATGAT 326
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Qy 105 ThrHisAsnHisAsnHisProLeuLeu---LysAspSerLeuSerSerThrLeuAlaCys 123
Db 441 -----CACACGATCAGTTGCTGATGAAGCCCAATCTCTTATCTACATTAGCATGT 491
Qy 124 IleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPhe 143
Db 492 GTTCTTACTCTTAAGCGGTGAATATTTGGCATGATCATATGACGAAGGCCCTTGATTTT 551
Qy 144 IleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnProSerProIleGlyPheAsp 163
Db 552 ATCAAGTCTAATATAGCTTCTGCTACTGATGAGAACCAACGTTCTCCGGTGGGATTTGAC 611
Qy 164 IleIlePheProGlyLeuLeuGluTyrAlaLysAsnAspIleAsnLeuSerLys 183
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; Sequence 23, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: B01378 US NA
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1049)
US-09-614-912-23
Alignment Scores:

Pred. No.: 5,54e-163 Length: 2403
 Score: 1523.00 Matches: 317
 Percent Similarity: 62.1% Conservative: 133
 Best Local Similarity: 43.7% Mismatches: 233
 Query Match: 37.0% Indels: 42
 DB: 3 Gaps: 8

US-10-041-018-383 (1-784) x US-09-614-912-23 (1-2403)

QY 90 IleAsnAsnGlnLeuAsnAspGlySerTrpGluLeuValAsnHisThrHisAsnHisAsn 109
 DB 12 CTCAGAACCCAGCAGATGATGATCTTGGGGTGC-----AGCCAATCTGAC 59
 QY 110 HisProLeuLeuLysAspSerLeuSerThrLeuAlaCysIleValAlaLeuLysArg 129
 DB 60 TCATCGGTACAGAGGATGTTCTTCATCCAGCTGGCATGTGTTCTTGGGTTGAAGA 119
 QY 130 TrpAsnValGluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAla 149
 DB 120 TGGAAATGTTGGCAGAGAGAACATTTGGAGAGGACTGCATTTTCATCGGAGGAATTTCTCT 179
 QY 150 SerAlaThrGluLysSerGlnProSerProIleGlyPheAspIleIlePheProGlyLeu 169
 DB 180 GTTGCTATGACGAGCAGTTCATCTCTATAGGTTTCAACTTCACCTTTCCTGTTG 239
 QY 170 LeuGluTyAlaLysAsnLeuAspIleAsnLeuLeuSerLysGlnThrAspPheSerLeu 189
 DB 240 CTTAGCCTCGGCATTGATGGGTTTAGAATTTCTGTAGACAAATTTGATGCTGTGGC 299
 QY 190 MetLeuHisLysArgGluLeuGluGlnLysArgCysHisSerAsnGluMetAspGly--- 208
 DB 300 ATTCTTTCACCGCCGGGAGATGGAATTCAAAAGGCTGGCTGTGATAGTTCTTTTGGAGA 359
 QY 209 -----TyrLeuAlaTyIleSerGluGlyLeuGlyAsnLeuTyAspTrpAsnMetVal 226
 DB 360 AAAGCATATATGCTTTTATCCAGAGGATGCGAATATATGCTGGAGTGGATCAAGTT 419
 QY 227 LysLysTyGlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAla 246
 DB 420 ATGAAAGTTTCAGAGGAGATGATGATCATTTGTTGAGCACTCTTCCCAACTGCTGTGCA 479
 QY 247 PheIleAsnHisGlnAsnProGlyCysLeuAsnTyIleAsnSerLeuLeuAspLysPhe 266
 DB 480 TTAATCCACAAATACACAGCACCAAGCCCTTCAATACCTAAATTTGCTTGTCAATGAATTT 539
 QY 267 GlyAsnAlaValProThrValTyProHisAspLeuPheIleArgLeuSerMetValAsp 286
 DB 540 GGCAGTGCAGTACCAAGATGATATCTTCAAGGGTACATTTGTCAGCTTTTCAATGGTGAC 599
 QY 287 ThrIleGluArgLeuGlyIleSerHisPheArgValGluIleLysAsnValLeuAsp 306
 DB 600 GCGCTTGAAAATGGAATTTCTCAGCGCTTTGTCAGTGAAATAGAAAGCATCTCTGGAC 659
 QY 307 GluThrTyArgCysTrpValGluArgAspGluGlnIlePheMetAspValThrCys 326
 DB 660 ATGCATACAAATGCTGGTTACAGAATGATGAGAACTCATGATGATGACATGCAATTT 719
 QY 327 AlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyGluValSerProAspProLeuAla 346
 DB 720 GCAATGGCATTTTCGCTTTTGGAGATGAATGGTTAGCATGTTTCTCAGATGAGCTGTCT 779
 QY 347 GluIleThrAsnGluLeuAla-----LeuLysAspGluTy 358
 DB 780 CAGTTGTCGGAGCTTCCATTTCCATGATTCATCAAGGATATTTAAATGATACAAA 839
 QY 359 AlaAlaLeuGluThrTyHisAlaSerHisIle---LeuTyGlnGluAspLeuSerSer 377
 DB 840 TCCCTACTGGAATTTGACAGACCTCAAAAGTACCTTATCAGAAACGATCTGATCTTA 899
 QY 378 GlyLysGlnIleLeuLysSerAlaAspPheLeuLysGluIleSerThrAspSerAsn 397
 DB 900 GATCGCATAGTTCTCTGGCTGGCAACTTATTTGAAGGATAAGATGTGCTAGTAGGTTG 959

QY 398 ArgLeuSerLysLeuIleHisLys----- 405
 DB 960 CAAAAGACATCGATTTTGGAGAGATGCTGCAACAAAATTTAAATCTCTATTTTACCTT 1019
 QY 406 -----GluValGluAsnAlaLeuLysPhePro 414
 DB 1020 GGAGGTTTCAGTTTATGCTGTGTTTGTGTTTTCAGATCGATGATGCTGTTAAATTTTCCC 1079
 QY 415 IleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyAsnValAsp 434
 DB 1080 TTGATTTCCACATCGGAGCGCTAGAACACAGAGAAACATCGAACATTTTGTATGCTTGG 1139
 QY 435 AsnThrArgIleLeuLysThrTyHisSerSerAsnIleSerAsnThrAspTyLeu 454
 DB 1140 GGTTCCTCTGATGCTA--ACAACAAAATCCTCATCTTTTGTATCATCAAGAATTCCTA 1196
 QY 455 ArgLeuAlaValGluAspPheTyThrCysGlnSerIleTyArgGluGluLeuLysGly 474
 DB 1197 GCTTTGGCAGTCCGAAGATTTCACTTCTCTCAACGTTTACCGGGATGAATTCGGCAT 1256
 QY 475 LeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThr 494
 DB 1257 CTTGATGTTGGTGAAGGAGAACAGCTGGACCACTCAATTTGCTCGGCAAACTG 1316
 QY 495 AlaTyCysTyThrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArg 514
 DB 1317 ACATATTTGCTATCTGCTGCTGCTACCGTATTTTCTCTGAATTTGCTGACGCTCGC 1376
 QY 515 IleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGly 534
 DB 1377 ATTTCATGGGCCAAAATGCTGCTCACAACCTGCTGATGACTTCTTCGATGTTGGT 1436
 QY 535 GlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspVal 554
 DB 1437 GGATCAAAAGAAATTTAGAAAACCTGATAGCACTAGTTGAGAAATGGCATGGGCACCAT 1496
 QY 555 AspLysAspCysCysSerGluHisValArgIlePheLeuAlaLeuLysAspAlaIle 574
 DB 1497 GCAGTTGAGTTCTATTTCGGAACAGGTGAAAATAGTATTTTCTGCTATTATACACAGTG 1556
 QY 575 CysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIle 594
 DB 1557 AACCATCTTGGAGCAATGCTTCTGCAGCACAAAGCGCTGATCTTACAAACCACTAGTA 1616
 QY 595 GlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAla 614
 DB 1617 GAAATGCTGGATTTGTTTAAAGTCTATGATGCTGAGGCAAGATGGCAGAGATGCCAA 1676
 QY 615 TyrValProThrLeuAsnGluTyMetGluAsnAlaTyValSerPheAlaLeuGlyPro 634
 DB 1677 TATGTACCAACAGTTGAGNAATACATGACAAATGCTGTTGCTCAITTTGACCTGGGCCA 1736
 QY 635 IleValLysProAlaIleTyPheValGlyProLysLeuSerGluGluIleValGluSer 654
 DB 1737 ATTGTCTCCAGCATTTGATTTTGTAGGCAAGAGCTATTAGAGCATGCTGTCAAAGAT 1796
 QY 655 SerGluTyHisAsnLeuPheLysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle 674
 DB 1797 GAAGATACGATAAAATTTATTTAGGCTAGTAGCAGCTTGGGGAGGCTCTCAATGATAC 1856
 QY 675 HisSerPheLysArgGluPheLysGluLysLeuAsnAlaValAlaLeuHisLeuSer 694
 DB 1857 CAAAGTTTAGAGGAGGAGCAACACAGGGGAGAGCTGAATAGTGTCTCTACTTGTGCTC 1916
 QY 695 AsnGlyLysGlyLysValGluGluValValGluGluMetMetMetMetMetLys 714
 DB 1917 CACAGTGGTGGTCTTATGTCCTAGAGCGCGCTAAAAGCAAGATGCAAGAGTCCATAGAC 1976
 QY 715 AsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProArg 734
 DB 1977 GTGCTAGAGGAGACTTGTAAAGTTGGTCTCAGGAAAGAA---AGTGTGTTCTTAGG 2033
 QY 735 AlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyAlaAsnAsp 754

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Db 2034 CCATGCAAGAGCTCTTCTGGAAGATGTGTAAAGATCTTCACTGTTTACTCTCAAGAT 2093
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Qy 755 AspGlyPheThrGly---AsnThrIleLeuAspThrValIleAspIleIleIleIleIleIle 773
      |||||::: ||||| ||||| ::|||::: |||||::: |||||::: |||||::: |||||:::
Db 2094 GATGATTTAGCTCCCAAGGAATGGTCAAGTGCAGTCAATGCTGTTATCAACAGGCCA 2153
      |||||::: ||||| ||||| ::|||::: |||||::: |||||::: |||||::: |||||:::
Qy 774 LeuValLeuValAsn 778
      |||::: |||||
Db 2154 CTCAAAGTCCAAAC 2168
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RESULT 4
US-10-041-007-1
; Sequence 1, Application US/10041007
; Patent No. 6946283
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; INVENTOR: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081051
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2705
; TYPE: DNA
; ORGANISM: ginkgo biloba
US-10-041-007-1

Alignment Scores:
Pred. No.: 8,08e-113 Length: 2705
Score: 1084.50 Matches: 266
Percent Similarity: 51.5% Conservative: 152
Best Local Similarity: 32.8% Mismatches: 330
Query Match: 26.4% Indels: 65
DB: 3 Gaps: 14

US-10-041-018-383 (1-784) x US-10-041-007-1 (1-2705)
Qy 10 ProLeuLeuThrIleSerAsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThr 29
      |||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 278 CCAGTGTCTGGAAGGACCATTCATCGACTCTTAACATCCCTAAATCCCAACGGACA 337
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 30 SerHisGlyGlyGlnThrAsnProThrAsnLeuIleAspThrThrIleAspThrIleArgIle 49
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 338 TCGAATCAAGCGTCGATGAGACATCAATAAAGATCCAGACATTTGGTGAAGGAATC 397
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 50 GlnLysGlnPheLysAsnVal-----GluIleSerValSerSerThrAspThrAla 66
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 398 CAGTGCATGTTTCAGTCCATGGCGGACGGTGAACCAATCCATCTCATATGATACAGCT 457
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 458 TGGGTGGCAAGATTCCTGTCATTTGACGGCTCTGGTGCACCCCAATTTCCCAACGCTT 517
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 87 AsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTyrIleGlyLeuValAsnHisThrHis 106
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 518 CAATGATTTCTGAACATCACTGCCAGATGGCTGCTGGGGT----- 559
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 107 AsnHisAsnHisProLeuLysAspSerSerThrLeuAlaCysIleValAla 126
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 560 GAGGAGTGCAATTTCTGCGGTATGACAGATTTTAAACACTCTCGCTGCTCCCTCACT 619
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSer 146
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 620 CTCAAATATGGAATAAGGCGGACATTCAGTGCAGAAAAGGGGTTCAGTTTGTGAGAAA 679
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 147 AsnLeuAlaSer---AlaThrGluLysSerGlnProSerProIleGlyPheAspIleIle 165
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 680 CACATGGAGAATGAAGACGAGCTGACATCAACAGGCAAGTGGATTCAGGTCGTG 739
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```

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Qy 166 PheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuLeuSerLysGlnThr 185
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Db 740 TTTCTCGCAATGTTAGATGAAGCAAAAAGCTTTGGGATTTGGATCTTCTTATCACCTCCCT 799
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 186 AspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLysArgCysHisSerAsnGlu 205
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 800 TTCATCTCCCAATCCACCAAAAGGCCAGAAAAGCTTCAAAAGATTTCCCTCATGT 859
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Qy 206 MetAspGlyTyr-----LeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAsp 222
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 860 CTTTCAACCATCAGACGGCGTGTCTACTCTCTGGAGGTTTGCAGAGTGTGGTGAC 919
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 223 TrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSerAla 242
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 920 TGGCAAGAGATCACAATCTTCAATCAAGAGACGGATCAATTTTAAGCTCCCTCGCATCT 979
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 243 ThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLeu 262
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 980 ACTGCTGTGCTTTCATGCACACTCAAAACAACGATGCTCACTTCTCACTTCTCACTTCG 1039
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 263 LeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArgLeu 282
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1040 CTCAGCAATTTGGCGACTACGTTCTTCCCATTTACCCACTTGTATCTATTGAACGCC 1099
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 283 SerMetValAspThrIleGluArgIleGlyIleSerHisPheArgValGluIleLys 302
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1100 TGGGCTGTGATACAGTTGAACGCTTGGGAATCGATCGTATTTTCAAGAAAGAAATCAAA 1159
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 303 AsnValLeuAspGluThrTyrArgCysTrp---ValGluArgAspGlu----- 317
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1160 GAATCTCTGGATTACGTTTATAGGTACTGGGACGGCAAGAGCGGTGGATGGGCAAGA 1219
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 318 ---GlnIlePheMetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsn 336
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1220 TGCATCTCTTCTCTGATGCGATGACACTGCCATGGGTCTTAGAATCTCTGAGACTTCAT 1279
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 337 GlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu----- 351
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1280 GGATCAATGTATCTTCAGATGTTCTGGAGAATTTTCAGAGCAGAGAAAGAGACTTCTTT 1339
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 352 -----LeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyr 364
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1340 TCGTTTGGCGGTCAACGCAATTTGGTGCACGATAAT-----CTTAACCTTTAT 1390
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 365 HisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSer 384
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1391 AGATGTTTCAAGTATGTTT-----CCGGAGAGAAAGATAATGAAGAA 1435
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 385 Ala-----AspPheLeuLysGluIleIleSerThrAsp 395
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1436 GCTAAGACCTTCACTACAAATCATCTCCAAATGCTTTGCCAAAACCAACGCAATTTGAT 1495
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 396 SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIle 415
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1496 AAGTGGCTGTCAAGAGGATCTTCTGAGAGGTGGAGTATGCTATAAGATATCCGTGG 1555
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 416 AsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyrAsnValAspAsn 435
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1556 CATAGAAGTATGCCAAGATTGGAGGCAAGAGTTACATAGAGCAATTTGGATCAATGAT 1615
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 436 ThrArgIleLeuLysThrThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArg 455
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1616 GTCTGGCTGGGAAGACTGTATAGATGCTATATGATGCTAGCAGCAACAAAATAATTTGGAG 1675
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 456 LeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeu 475
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1676 CTGGCCAAATTTGACTTCAATATGTTGTCAGGCTTACACCAAAAGAGGACTCAACACATT 1735
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 476 GluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAla 495
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1736 GTCAGCTGTTGGAGAGAAATCGGATTCATATGATCTTACATTCACCGCCAGCGGCTGTG 1795
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QY 496 TyrCysTyrPheSerValAlaThrLeuSerSerProGluLeuSerAspAlaArgile 515
Db 1796 GAAATGTTATTTCTCAGTGGCGTTAGTATGTTTGGAGCCAGAAATTCGCTGCTTGTAGAAAT 1855
QY 516 SerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGly 535
Db 1856 GCCTATGCCAAGACTTCTCCCTCGCAGATTATTTCTAGACGATCTTTACGACACCCACGGA 1915
QY 536 ThrIleAspGluLeuThrAsnLeuLeuGlnCysValGluLeuTrpAsnValAspValAsp 555
Db 1916 TCCTGTGATGATCTTAATATGTTCTCTGAAGCGTCCGAAGATGGGATATCTCTGTGCTG 1975
QY 556 LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys 575
Db 1976 GATAGCGTTCGGGATATCAGTTGAAAGTTTGTCTCTAGGGCTGTACACACACAGTGAAT 2035
QY 576 TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln 595
Db 2036 GGATTTGGAAAGATGACTCAAGGAACAAGCGCGTGATGCTGGGCTATCTTCGAAAA 2095
QY 596 ThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr 615
Db 2096 GTATGGAGGCGTGTCTCGCATCGTATACCAAGAGCCGAATGTCGGCAGCAAGTAT 2155
QY 616 ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle 635
Db 2156 GTCCGACATTCACGAATATGTGGAATATGCCAAGTGTCCATAGCACTTGCACAGTC 2215
QY 636 ValLysProAlaIleTyrPheValGlyProLysLeuSerGluGluIleValGluSerSer 655
Db 2216 GTACTAACTCAATCTTTTCACTGGAGAAATTACTTCTGATTTACATTTTACAGCAAGTA 2275
QY 656 GluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle 674
Db 2276 GACTTCGGGCCAAATTTCTGCATCTTGTCTTGTGACTGACGACTTAATCAATGACACC 2335
QY 675 HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSer 694
Db 2336 AAGACTTACCAGCGCGAGAGAAACCGTGGTGAATTTGTTTCCAGCGTACAGTG-CTACAT 2394
QY 695 AsnGlyCysSerGlyLys-ValGluGluGluValValGluGluMetMetMetMetIle 714
Db 2395 GAGGGAATATCCGAGTGACACAGAGGAAGAGCTCTAAGTCATGTTTATGGTATCATCGA 2454
QY 714 AsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProAr 734
Db 2455 CAACGCACTGAAGGAATTG---AATTGGGAGTTGGCCAAACCCAGCGAGCAATGCCCAT 2511
QY 734 GAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs 754
Db 2512 GTGTGTGAGAGACTGCTGTTCAACACTGCAAGAGTGATGACGCTGTTTATATGTACAG 2571
QY 754 pAspGlyPhe-----ThrGlyAsnThrIleLeuAs 764
Db 2572 AGATGGCTTTGGTATCTCTGACAAAGAGATGAAAGACCATGTGACGCGCAACTCTTTTGA 2631
QY 764 pThrVal-----LysAspIleIleTyrAsn 772
Db 2632 TCCTGTGGCGTAGCATCTACTGATATATATATATAT 2665
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RESULT 5

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US-10-041-007-36
; Sequence 36, Application US/10041007
; Patent No. 6946283
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
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; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 2388
; TYPE: DNA
; ORGANISM: Ginkgo biloba
US-10-041-007-36

Alignment Scores:
Pred. No.: 7 93e-112 Length: 2388
Score: 1075.00 Matches: 261
Percent Similarity: 52.1% Conservative: 157
Best Local Similarity: 32.5% Mismatches: 332
Query Match: 26.1% Indels: 54
DB: 3 Gaps: 13
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US-10-041-018-383 (1-784) x US-10-041-007-36 (1-2388)

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QY 10 ProLeuLeuThrLysSerAsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThr 29
Db 22 CCAGCTGTCTGGAAGGACGATTTTCATCGACTCTCTAACATCCCTTAATTCACGCGACA 81
QY 30 SerHisGlyGlyGlnThrAsnProThrAsnLeuIleAspThrThrLysGluArgIle 49
Db 82 TCGAAATCAAGCGTCGATGAGACAATCAATAAAAGAAATCCAGACATTTGGTGAAGGAATC 141
QY 50 GlnLysGlnPheLysAsnVal-----GluIleSerValSerSerTyrAspThrAla 66
Db 142 CAGTGCATGTTTCAGTCCATGGGCGGAGCGTGAACGAATCCATCTGCATATGATACAGCT 201
QY 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
Db 202 TGGGTGCGAAGATTCGTCATTTGACGGCTCTGTGTGACCCCAATTTTCCCAACGCTT 261
QY 87 AsnTrpLeuLeuAsnAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
Db 262 CAATGGATTCGAACAATCAACTGCCAGATGGCTGCGTGGGT----- 303
QY 107 AsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThrLeuAlaCysIleValAla 126
Db 304 GAGGAGTGCAATTTTCTGGCGTATGACAGATTTTAAACACTCTGCGCTCCCTCCTCACT 363
QY 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSer 146
Db 364 CTCAAATATGGAATAAGGCGACATTCAGTCCAGAAAGGGGTGATTTGTGAGAAA 423
QY 147 AsnLeuAlaSer---AlaThrGluLysSerGlnProSerProIleGlyPheAspIle 165
Db 424 CACATGGAAGAAATGAAGGACGAGCTGACAATCACAGGCCAAGTGGATTCGAGGTGCTG 483
QY 166 PheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuSerLysGlnThr 185
Db 484 TTTCTTGCATATGTTAGTGAAGCAAAAGCTTGGGATTTGGATCTCTCTTATACCTCCCT 543
QY 186 AspPheSerLeuMetLeuHisLysArgGluLeuGlnLysArgCysHisSerAsnGlu 205
Db 544 TTTCTTCCCAATCCCAAAAGCCGAGAAAAGCTTCAAAAGATTCCTCCCTCAATGTT 603
QY 206 MetAspGlyTyr-----LeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAsp 222
Db 604 CTTTCAATACCATCAGACGCGTGTGCTCTACTCTCTGAGGGTTTGAAGATGTGGTGGAC 663
QY 223 TrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSerAla 242
Db 664 TGGCAAGAGATCAAAATCTTCAATCAAGAGACGGATCATTTTAAAGTCCCTCCCTGCACT 723
QY 243 ThrAlaAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLeu 262
Db 724 ACTGCTGTGTCTTTCATGACACTCAAAACAAACGATGCTCCACTTCTCACTTCCTCGTG 783
QY 263 LeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArgLeu 282
Db 784 CTCGCAAAATTTGGCGACTACGTTTCTTGTGCAATTAACCACTTGATCTATTATGAACGCTC 843
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Qy	283	SerMetValAspThrIleGluArgLeuGlyIleSerHisSheArgValGluIleLys	302
Db	844	TGGGCTGTCGATACAGTGAACGCTGGGAATCGATCGCTATTTCAGAAAGAAATCAAA	903
Qy	303	AsnValLeuAspGluThrTyArgCysTyr---ValGluArgAspGlu---	317
Db	904	GAATCTCTGGATTACGTTTATAGGTACTGGGACGCCGGAAGAGCGCTGGGATGGCAAGA	963
Qy	318	---GlnIlePheMetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsn	336
Db	964	TGCAATCCTATTCTTGATGTCGATGACACTGGCCATGGGTCTTAGNATCTCTGAGACTTCAT	1023
Qy	337	GlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu---	351
Db	1024	GGATACAATGTATCTTCAGATGTTCTGGAGAAATTCAGAGACGACGAGAAAGGAGACTCTCTT	1083
Qy	352	-----LeuAlaLeuLeuAspGluTyArgAlaLeuGluThrTyr	364
Db	1084	TGCTTTGCCGGTCAAACGCAATTTGGTGACCGATAAT-----CTTAACCTTTTAT	1134
Qy	365	HisAlaSerHisIleLeuTyGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSer	384
Db	1135	AGATGTTTCAAGTATGTTT-----CCGGGAGAAAAGATAATCGGAAGAA	1179
Qy	385	Ala-----AspPheLeuLysGluIleIleSerThrAsp	395
Db	1180	GCTAAGACCTTCTACTACAAATCATCTCCAATAATGCTCTTGCCAAAACAACGCAATTTGAT	1239
Qy	396	SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIle	415
Db	1240	AAGTGGCGTCTCAAGAAGAGTCTTCTCGGAGAGGTGGAGTATGCTATAAAGTATTCGTGG	1299
Qy	416	AsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeuTyArgAsnValAspAsn	435
Db	1300	CATAGAAGTATGCCAAGATTGGAGGCAAGAAATTACATAGACAAATTTGGATCAAAATGAT	1359
Qy	436	ThrArgIleLeuLysThrTyHisSerSerAsnIleSerAsnThrAspTyrLeuArg	455
Db	1360	GTCTGGCTGGGGAAGACTGTGTAAAGATGCTATATGTGACCAACGAAAAATAATTTGGAG	1419
Qy	456	LeuAlaValGluAspPheTyThrCysGlnSerIleTyArgGluGluLeuLysGlyLeu	475
Db	1420	CTGGCCAAATTGGACTCAATATGGTCGACGGCTTACRCCAAAAGGAGACTCAACACATT	1479
Qy	476	GluArgTyrValValGluAsnLysLeuAspGlnLeuLysPheAlaArgGlnLysThrAla	495
Db	1480	GTACGCTGGTGGAGAGAATCGGGATTCAATGATCTTACATTCCCGCCGACGCGCTGTG	1539
Qy	496	TyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIle	515
Db	1540	GAATGTATTCTCAGTGGCGGTAGTATGCTTTGAGCCAGAAATTCGCTGCTTAGAAT	1599
Qy	516	SerTyrAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGly	535
Db	1600	GCTATGCCAAGACTCTTCGCTCGCAGTTATTCAGACCATCTTTACGACACCCACCGA	1659
Qy	536	ThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyrAsnValAspValAsp	555
Db	1660	TCTCTGGATGATCTTAAATTTGTTCTCTGAAGCGGTCCGAAAGATGGGATATCTCTGTGCTG	1719
Qy	556	LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys	575
Db	1720	GATAGCGTTCCGGATNAATCAGTTGAAGTTTGTCTCTAGGCTGTACAACACAGTGAAT	1779
Qy	576	TripIleGlyAspGluAlaPheLysTyrGlnAlaArgAspValThrSerHisValIleGln	595
Db	1780	GGATTTGGAAAAGATGGACTCAAGGAACAAGCGCGTATGCTGTGGCGCTATCTTCGAAA	1839
Qy	596	ThrTyrLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyrThrArgAspAlaTyr	615
Db	1840	GTATGGAGGGCTTGTCTCGATCGTATPACAAAAGACCGAAATGGTTCGGAGCAAAAGTAT	1899

Qy	616	ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle	635
Db	1900	GTGCCGCAATTCAACGAATATGTGGAATAATGCGAAAGTGTCCATAGCATTGCGCAGTC	1959
Qy	636	ValLysProAlaIleTyrPheValGlyProLysLeuSerGluLurleValGluSerSer	655
Db	1960	GTACTAAACTCAATCTTTTTCACCTGGAGAATTACTTCCTGATTTACATTTTACACCAAGTA	2019
Qy	656	GluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIle	674
Db	2020	GACCTTCGGTCCAAATTTCTGCACTCTTGTCCTTTGACTGGACGACTAATCAATGACACC	2079
Qy	675	HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValaLeuHisLeuSer	694
Db	2080	AAGACTTACCAGCGCGAGAGAAAACCGTGGTGAATTGGTTTCCAGCGTACAGTG-CTACAT	2138
Qy	695	AsnGlyCysSerGlyLys-ValGluGluGluValValGluGluMetMetMetIleLys	714
Db	2139	GAGGGAAATCCCGAGTGCACAGAGGAAGCTCTAAAGTCATGTTATGGTATCATCTCGA	2198
Qy	714	AsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlySerIleValProAr	734
Db	2199	CAAGCACTCAAGGAATTG---AATTGGGAGTTGGCCACCCAGCAGCAATGCCCCATT	2255
Qy	734	GalaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs	754
Db	2256	GTGTGTGAGAAGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATGTACAG	2315
Qy	754	pAspGlyPhe-----ThrClyAsnThrIleLeuAspThrValLysAspIleIleTyrAs	772
Db	2316	AGATGGCTTTGGTATCTCTGACAAAGAGATGAAGACCATGTCCGCCGAACACTCTTTTCGA	2375
Qy	772	ProLeu 774	
Db	2376	TCTGTG 2382	
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US-10-041-007-34			
; Sequence 34, Application US/10041007			
; Patent No. 6946283			
; GENERAL INFORMATION:			
; APPLICANT: Matsuda, Seiichi P.T.			
; APPLICANT: Schepmann, Hala G			
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthese			
; FILE REFERENCE: P02081US1			
; CURRENT APPLICATION NUMBER: US/10/041,007			
; CURRENT FILING DATE: 2002-01-07			
; PRIOR APPLICATION NUMBER: US 60/259,881			
; PRIOR FILING DATE: 2001-01-05			
; NUMBER OF SEQ ID NOS: 41			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 34			
; LENGTH: 2445			
; TYPE: DNA			
; ORGANISM: Ginkgo biloba			
US-10-041-007-34			
Alignment Scores:			
Pred. No.: 8.25e-112 Length: 2445			
Score: 1075.00 Matches: 261			
Percent Similarity: 52.1% Conservative: 157			
Best Local Similarity: 32.5% Mismatches: 332			
Query Match: 26.1% Indels: 54			
DB: 3 Gaps: 13			
US-10-041-018-383 (1-784) x US-10-041-007-34 (1-2445)			
Qy	10	ProLeuLeuThrLysSerAsnArgProAlaAlaLeuSerAlaIleHisThrAlaSerThr	29
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Qy	30	SerHisGlyGlnThrAsnProThrAsnLeuIleAspThrThrLysGluArgIle	49

Db 139 TCGAATCAAGCGTCGATGACACAATCAATAAAGAAATCCAGACATTTGGTGAAGGAATC 198
Qy 50 GlnLysGlnPheLysAsnVal-----GlnLysSerValSerSerTyrAspThrAla 66
Db 199 CAGTGCATGTTTCAGTCCATGGGCGCGGTAAGAAATCCATCTGCATATGATACAGCT 258
Qy 67 TrpValAlaMetValProSerProAsnSerProLysSerProCysPheProGluCysLeu 86
Db 259 TGGGTGGCAAGAATTCGCTCAATGACGGCTCTGGTCGACCCCAATTTCCCAACGCTT 318
Qy 87 AsnTrpLeuLeuAsnGlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHis 106
Db 319 CAATGGATTCGAACAATCAACTGCCAGATGGCTCGTGGGGT----- 360
Qy 107 AsnHisAsnHisProLeuLeuLysAspSerSerThrLeuAlaCysIleValAla 126
Db 361 GAGGAGTGCATTTTCTGGCGTATGACAGAGTTTAAACACTCTCGCTCCCTCACT 420
Qy 127 LeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSer 146
Db 421 CTCAAAATATGGAATAGGCGGACATTCAGTGCGAAGAGGGGTGAGTTTGTGAGAAA 480
Qy 147 AsnLeuAlaSer---AlaThrGluLysSerGlnProSerProIleGlyPheAspIleIle 165
Db 481 CACATGGAAGAAATGAAGGACGAGCTGACAAATCACAGGCGCAAGTGGATTGAGGTG 540
Qy 166 PheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsnLeuSerLysGlnThr 185
Db 541 TTTCTCGCAATGTTAGATGAAGCAAAAGCTTGGATTGGATCTCTTATCATCCTCCCT 600
Qy 186 AspPheSerLeuLeuHisLysArgGluLeuGlnLysArgCysHisSerAsnGlu 205
Db 601 TTCATCTCCCAATCCACAAAGCGCCAGAAAAGCTTCAAGAGATTCCTCAATGTT 660
Qy 206 MetAspGlyTyr-----LeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAsp 222
Db 661 CTTCAATACCATCAGACGGCGTGTCTACTCTCTGAGGGTTTGCAGATGTGGTGAC 720
Qy 223 TrpAsnMetValLysLysTyrGlnMetLysAsnGlySerValPheAsnSerProSerAla 242
Db 721 TGGCAAGATATCAAAATCTTCAATCAAGAGCGGATCATTTTAAAGCTCCCTCGCATCT 780
Qy 243 ThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLeu 262
Db 781 ACTGCTGTGCTCTCATGCACACTCAAAACAAACGATGCTCCACTTCTCACTTCGTG 840
Qy 263 LeuAspLysPheGlyAsnAlaValProThrValTyrProHisAspLeuPheIleArgLeu 282
Db 841 CTCAGCAAAATTTGGCGACTACGTTCTTGGCAATACCCACTTGATCTATTTGAACGCTC 900
Qy 283 SerMetValAspThrIleGluArgLeuGlyLysSerHisPheArgValGluIleLys 302
Db 901 TGGGCTGTGCATACAGTTGAACCTTGGGAATCGATCGCTATTTCAGAAAGAAATCAAA 960
Qy 303 AsnValLeuAspGluThrTyrArgCysTrp---ValGluArgAspGlu----- 317
Db 961 GAATCTCTGATTTACGTTTATAGTACTGGGCGCCGAAAGAGCGGTGGGATGGCGAGA 1020
Qy 318 ---GlnIlePheMetAspValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsn 336
Db 1021 TGCATATCTTCTGATGTCGATGACACTGCCATCGGCTTGTAGATCTCTGAGACTTCAT 1080
Qy 337 GlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu----- 351
Db 1081 GGATACAAATATCTTCCAGATGTTCTGGAGAAATTTTCAGACAGCAGAAAGAGACTTCTTT 1140
Qy 352 -----LeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyr 364
Db 1141 TGCCTTGGCCGTCAAACGCAAAATGGTGTGACCGATAAT-----CTTAACCTTTAT 1191
Qy 365 HisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLysGlnIleLeuLysSer 384
Db 1192 AGATGTTTCAAGATATGTTT-----CCGGGAGAGAAAGATAATGGAAGAA 1236

Qy 385 Ala-----AspPheLeuLysGluIleIleSerThrAsp 395
Db 1237 GCTAAGACCTTCACTACAATCATCTCCAAATGCTCTGCCAAAACAACGCAATTTGAT 1296
Qy 396 SerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAlaLeuLysPheProIle 415
Db 1297 AAGTGGGCTCTCAAGAGGATCTTCTCTGGAGAGGTGGAGTATGCTATAAAGTATCCGTGG 1356
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Db 1357 CATAGAAGTATGCCAAGATTGGAGGCAAGAGTTTACATAGCAATTTGGATCAATGAT 1416
Qy 436 ThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArg 455
Db 1417 GTCTGGCTGGGGAAGACTGTGTATAGATGCTATATGTGACCAACGAAAATATTTGGAG 1476
Qy 456 LeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGluGluLeuLysGlyLeu 475
Db 1477 CTGGCCAAATTTGGACTTCAATATGGTGCAGGCTTACACCAAAAGGAGACTCAACACATT 1536
Qy 476 GluArgTrpValGluAsnLysLeuAspGlnLysPheAlaArgGlnLysThrAla 495
Db 1537 GTCAGCTGGTGGAGAGATCGGATTCATATGATCTTACATTACCCCGCAGCGCTGTG 1596
Qy 496 TyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIle 515
Db 1597 GAATGTATTTCTCAGTGGCGGTGTATGTGTTGAGCCAGAAATCGCTGCTGTAGAAAT 1656
Qy 516 SerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhePheAspIleGlyGly 535
Db 1657 GCCTATGCCAAGACTTCTTGGCTCGCAGTTTATTTCTAGACGATCTTTACGACACCCACGA 1716
Qy 536 ThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAsp 555
Db 1717 TCTCTGGATGATCTTAAATTTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTCTG 1776
Qy 556 LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys 575
Db 1777 GATAGGTTGGGATTAATCGTTGAAAGTTTGTCTTCTAGGGCTGTACACACAGTGAAT 1836
Qy 576 TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln 595
Db 1837 GGATTTGGAAAGATGAGACTCAAGGAACAAGCGCGTGTGTCTGGGCTATCTTCGAAAA 1896
Qy 596 ThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr 615
Db 1897 GTATGGGAGGCTTGTCTGCATCGTATACCAAGAAAGCCGAATGGTCGGCAGCAAGTAT 1956
Qy 616 ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle 635
Db 1957 GTCCGACATTCACGAATATGGAATAATGCCAAAGTGTCCATAGCACTGGCAGCATG 2016
Qy 636 ValLysProAlaIleTyrPheValGlyProLysLeuSerGluGluIleValGluSerSer 655
Db 2017 GTACTAACTCAATCTTTTCACTGGAGAATTAATCTTCTGATTTACATTTTACGCAAGTA 2076
Qy 656 GluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArgIleLeuAsnAspIle 674
Db 2077 GACCTTTCGGTCCAAATTTCTGCATCTTGTCTTGTGACTGGACGACTAATCAATGACACC 2136
Qy 675 HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSer 694
Db 2137 AAGCTTTACCGCCGCGGAGAAACCGTGGTGAATGTGTTTCCAGCGGTACAGTG-CTACAT 2195
Qy 695 AsnGlyGluSerGlyLys-ValGluGluValValGluGluMetMetMetMetIleLys 714
Db 2196 GAGGGAATTCGGAGTGCACAGGAGGAAGCTCTAAGTCAATGTTTATGTGATCATCGA 2255
Qy 714 sAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsnGlnSerIleValProAr 734
Db 2256 CAACGCACTCAAGGAATG---AATTTGGAGATTGGCCCAACCCAGCGAGCAATCCCATTT 2312

QY 496 TyxCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIle 515
 Db 1774 GAATGTATTTCTCAGTGGCGGTAGTATGTTGAGCCAGATTCGCTGCTTAGATTT 1833
 QY 516 SerTrpAlaLysAsnGlyIleLeuThrThrValValAspPhePheAspIleGlyGly 535
 Db 1834 GCCTATGCCAAGACTTCTTCCCTCGCAGTATTATCTAGACGATCTTTACGACACCCGGA 1893
 QY 536 ThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrpAsnValAspValAsp 555
 Db 1894 TCTCTGATGATCTTAATTTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTG 1953
 QY 556 LysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCys 575
 Db 1954 GATAGCGTTCGGGATAATCAGTTGAAAGTTTGGTCTCTAGGGCTGTACACACAGTGAAT 2013
 QY 576 TrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThrSerHisValIleGln 595
 Db 2014 GGATTTGGAAAGAGTGAAGTCAAGGAACAAGCGGTGATGTGCTGGGCTATCTTCGAAA 2073
 QY 596 ThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyr 615
 Db 2074 GTATGGAGGGCTTGTCTCGATCGTATACCAAGAAGCCGAATGGTGGCAGCAAGATAT 2133
 QY 616 ValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIle 635
 Db 2134 GTCCCGACATCAACGATATGCGAAATGCGAAATGCCAAGTGTCCATGACACTTGGCAGTC 2193
 QY 636 ValIleProAlaIleTyrPheValGlyProLysLeuSerGluGluIleValGluSerSer 655
 Db 2194 GTACTAAACATCAATCTTTTCACTGGAGAAATTAATCTCTCATTTACATTTTACAGCAAGTA 2253
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 Db 2254 GACCTTGGGTCCAAATTTCTGCAATCTGTCTCTTGTGACTGGACGACTTAATCAATGACAC 2313
 QY 675 HisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSer 694
 Db 2314 AGACTTACACGCGCGAGAAACCGGTGGTAATGGTTTCCAGCGTACAGTG-CTACAT 2372
 QY 695 AsnGlyLysSerGlyLys-ValGluGluGluValValGluMetMetMetMetIleIle 714
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 QY 734 gAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAs 754
 Db 2490 GTGTGTGAGAGACTGCTGTTCAACTGCAAGAGTATGACCTGTTTATATGTACAG 2549
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RESULT 8

US-09-398-395A-55
 ; Sequence 55, Application US/09398395A
 ; Patent No. 6468772
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 64687721, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/398,395A

; CURRENT FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 55
 ; LENGTH: 2861
 ; TYPE: DNA
 ; ORGANISM: Abies grandis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (3)...(2606)
 ; OTHER INFORMATION: abietadiene synthase
 ; US-09-398-395A-55

Alignment Scores:
 Pred. No.: 2 89e-110 Length: 2861
 Score: 1062.50 Matches: 261
 Percent Similarity: 50.6% Conservative: 148
 Best Local Similarity: 32.3% Mismatches: 339
 Query Match: 25.8% Indels: 61
 DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-398-395A-55 (1-2861)

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 Db 297 ATCGATTCTCTAACGTCATCTCAAGGTTGCGAGCATCAGACGAGAAGCGT---ATCGAG 353
 QY 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
 Db 354 ACATTAAATATCCGAGATTGAAGATATGTTTAGATGTATGGGCTATGGCGAAACGAATCCC 413
 QY 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
 Db 414 TCTGCATATGACACTCTTGGGTAGCAAGGATTTCCAGCAGTTCATGCTCTGCAACACCT 473
 QY 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
 Db 474 CACTTTCTCGAGACGGTTGAATGGATTCTTCAAAATCAGTTGAAAGATGGGTCTTGGGT 533
 QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerSerSerThr 120
 Db 534 -----GAAGGATTCTTCTTGGCATATGACAGAAATCTGATCTAGTCCGCTACA 575
 QY 121 LeuAlaCysIleValAlaLeuLysAspTrpAsnValGlyGluAspGlnIleAsnLysGly 140
 Db 576 CTTGCATGTATTATTACCTTACCTCTCGCGTACTGGGAGACACAAGTACAGAAAGGT 635
 QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
 Db 636 ATTGAATTCTTCAGGACACAAGCTGGAAAGATGGAAGATGAAGCTGATAGTCTATAGGCCA 695
 QY 160 IleGlyPheAspIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
 Db 696 AGTGGATTGAAATAGTATTCTTCGCAATGCTAAGAAAGCTAAATCTTAGGCTTGGAT 755
 QY 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLys 199
 Db 756 CTGCCTTACGATTTGGCCATTCTCGAAACAATCATCGAAAGCGGGAGGCTAGACTTAA 815
 QY 200 ArgCysHisSerAsn-----GluMetAspGlyTyrLeuAlaTyrIleSerGluGly 216
 Db 816 AGGATCCCACTGATGTTCTCTATGCTTCCCAACAACGTTATGTATTCTTTTGGAAAGGT 875

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QY 217 LeuGlyAsnLeuTyrAspTrpAsnMetValLysLysTyrGlnMetLysAsnGlySerVal 236
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 876 TTACAAGAAATAGTAGCTGGCAGAAATAATGAACCTTCATCCAGGATGATCATTT 935

QY 237 PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 936 CTCAGCTCTCCGCACTACAGCGCTGTATTCATCGGTACAGGGAACAAAAGTGTG 995

QY 257 AsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHis 276
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 996 GATTTCTTGAACCTTGTCTTGAAGAAATTCGAAACCATGTGCTTGTCACTATCGCTT 1055

QY 277 AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHis 296
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1056 GATCTATTGAACTTTGTGGCGGTGTATACAGTTGACGGCTAGGTATCGATCGTCAT 1115

QY 297 PheArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTrpValGluArgAsp 316
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1116 TTCAAGAGGAGATCAAGGAACATTTGATTTATGTTTACAGCATTGGGACGAGAGGC 1175

QY 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1176 ATTGGATGGCGAGAGAGAATCTGTCTCTGATATTGATGATACAGCCATGGCGCTTCGA 1235

QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1236 ATCTTGAGATTACATGGATCAATGATCTCCAGATGTTTAAACAACATTTAGAGATGAG 1295

QY 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1296 -----AATGGGAGTCTTTGCTTCTTGGTCAAAACACAGAGAGGATTACAGAC 1346

QY 361 ----LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1347 ATGTTAAACGTCATCGTTGTTTCACATGTTTCATTT-----CCGGGAGAA 1391

QY 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1392 ACGATCATCGAAGAGCAAACTCTGTACGAAAGGTATCTGAGGAATGCTCTGAAAT 1451

QY 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1452 GTGGATGCCCTTGGACAAATGGCGCTTTAAAGAATATTCGGGAGAGGTAGATGCA 1511

QY 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1512 CTCAAATATCCCTGGCATAAGAGTAGTACCAAGTTGGAGGCTAGAAGCTATATTGAAAC 1571

QY 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsn 450
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1572 TATGGCCAGATGATGTGGCTTGGAAAACTGTATATATGATGATCCATACATTTTGGAT 1631

QY 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
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Db 1632 GAAAAGTATTAGAACTACGAAACTGGACTTCATAAAGGTGCAGTCTATACCAACCA 1691

QY 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAla 490
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1692 GAGCTTCAAGATCTTCGAAGTGGTGGAAATCATCCGGTTTCACGGATCTGAATTTCACT 1751

QY 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
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Db 1752 COTGACGGTGTGACGGAATATATTCTCACCGGCATCTTTATCTTTGAGGCCGAGTTT 1811

QY 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuLeuThrThrValValAspAspPhe 530
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 1812 TCTAAGTCGAGAGAGGTTTATACAAAACCTTCCAATTTCACTGTTATTAGATGATCTT 1871

QY 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
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QY 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuAlaLeu 570
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Db 1932 GATCTATCACTA--GTGACCAAAATGCCAACAAATCAAAATATGTTTGTGGGTTTC 1988
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QY 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1989 TACAATACTTTTAATGATATAGCAAAAGAGGACGTGAGAGGCAAGGGCGCGATGTGCTA 2048

QY 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2049 GGCTACATTCAAAATGTTTGGAAAGTCCAACTTGAAGCTTACACGAAAGAACAGAAATGG 2108

QY 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 2109 TCTGAAGCTAAATATGTGCCATCTCTCAATGAATATACATAGAGAATGCGAGTGTGTCAATA 2168

QY 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 2169 GCATTTGGGAACAGTCTGTTCTATTAGTGTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228

QY 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
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Db 2229 GTACTCTCCAAATTTGATCGCAATCTAGATTTCTTCAACTCATGGGCTTAAACAGGCGT 2288

QY 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 2289 TTGGTGAATGACACCAAACTTATCAGGCAGAGAGGTCAGAGTGAGTG--GCTTCT 2345

QY 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
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Db 2346 GCCATCAATGTTATGAAGGACCATCTTAAATCTCTGAAGAAGAGCTCTACAACAT 2405

QY 709 MetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
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Db 2406 GTCTAGTGTCTCGAAATGCCCCTCGAAGAGTTGAATAGG-----GAGTTTGTG 2456

QY 729 GlySerIleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHisValLeuAsn 748
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Db 2457 AATACAAAATACCGGATATTTACAAAGACTGGTTTGTGAACCTGCAAGAATATGCAA 2516

QY 749 PhePheTyrAlaAsnAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
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Db 2517 CTCCTTTTATCAAGGAGTGTGTTGACACTATCACATGATATGGAATTAAGAGCAT 2576

QY 766 ValLysAspIleIleTyrAsnProLeu 774
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Db 2577 GTCAAAAATTCCTCTCTTCCAACCGTT 2603

RESULT 9
US-09-887-586A-55
; Sequence 55, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-887-586A-55

Alignment Scores:
Pred. No.: 2,896-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-887-586A-55 (1-2861)

QY 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
DB 237 CTTTCCTTCTTCAATTTGGTGAACGAGAAATTCCTCCAGGATTTTGGAAAGGATGATCTT 296
QY 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
DB 297 ATCGATCTCTAAGCTCATCTCACAGGTTGCAGCATCACAGAGAGCGT---ATCGAG 353
QY 44 ThrThrysgluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
DB 354 ACATTAATATCCGAGATTAAAGAAATATGTTTAGATGTATGGCTATGGCGAAACGAAATCCC 413
QY 61 SerSerThrAspThrAlaTTPValAlaMetValProSerProAsnSerProLysSerPro 80
DB 414 TCTGCATATACACCTGCTGGGTAGCAAGATTCCAGCAGTTCAGCAGTTCGCAACCCCT 473
QY 81 CysPheProGluCysLeuAsnTTPLeuIleAsnAsnGlnLeuAsnAspGlySerTTPGly 100
DB 474 CACTTTCCTGAGCGGTTGAATGATGATCTTCAAAATCAGTTGAAGATGGGTCTTGGGT 533
QY 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLysSerThr 120
DB 534 -----GAAGGATTCCTACTTCTTGGCATATGACAGAACTAGCTGCTGCTACA 575
QY 121 LeuAlaCysIleValAlaLeuLysArgTTPAsnValGlyGluAspGlnIleAsnLysGly 140
DB 576 CTTGCGATGATTATTAATCCCTTACCCTCTGGCGTACTGGGGAGACACAAAGTACAGAAAGT 635
QY 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
DB 636 ATTGAATCTTCAGGACACCAAGCTGGAAAGATGGAAGTGAAGTGAAGTGAAGTGAAGTGA 695
QY 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
DB 696 AGTGGATTGCAATAGTATTTCTTCAATGCTTAAAGGAAGCTTAAATCTTTAGGCTTGAT 755
QY 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisLysArgGluLeuGluGlnLys 199
DB 756 CTGCTTTACGATTTGGCATTTCTTCAAAACAAATCATCGAAAGCGGGAGGCTAAGCTTTAA 815
QY 200 ArgCysHisSerAsn-----GluMetAspGlyTyrLeuAlaTyrIleSerGluGly 216
DB 816 AGGATTCCTGATGTTCTATGCTTCCCAACAGTTATGTTATTTTGGAAAGGT 875
QY 217 LeuGlyAsnLeuTyrAspTTPAsnMetValLysLysTyrGlnMetLysAsnGlySerVal 236
DB 876 TTACAGAATAATAGTAGTCTGCGAGAAAATAATGAACTTCAATCCAGGATGATCATTT 935
QY 237 PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
DB 936 CTCAGCTCTCGGCATCTACAGCGGCTGTATTCATGCGTACAGGGAACAAAAGTGTCTG 995
QY 257 AsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHis 276
DB 996 GATTTCCTTGAACTTGTCTTGAAGAAATTCGGAACCATCGTCCCTTCTCATATCCGCTT 1055
QY 277 AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHis 296

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DB 1056 GATCTATTTGAACGCTTTGTGGCGGTTGATACAGTTGAGCGGCTAGGTATCGATCGTCAT 1115
QY 297 PheArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTTPValGluArgAsp 316
DB 1116 TTCAAAGAGGATCAAGAGCATTGGATTATGTTTACAGCCATTGGGACGAAGAGGC 1175
QY 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
DB 1176 ATTGGATGGCGAGAGAGAATCTGTTCTGATATTGATGATACAGCCATGGGCTTTCGA 1235
QY 332 LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
DB 1236 ATCTTGAGATTACATGATCAATGATCTCTCAGATGTTTAAATAACATTAGAGATGAG 1295
QY 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
DB 1296 -----AATGGGAGTTCTTTTCTGCTTCTGGTCAACACAGAGAGAGTTACAGAC 1346
QY 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
DB 1347 ATGTTAAACGTCAATCGTTGTTCCATGTTTCAATTT-----CCGGGAGAA 1391
QY 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
DB 1392 ACGATCATGGAAGAACAAACTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAAT 1451
QY 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
DB 1452 GTGGATGCTTTCACAAATGGGCTTTTAAAGAATAATTCGGGAGAGGTAGATATGCA 1511
QY 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
DB 1512 CTCAATATATCCCTGGCATAAGAGTATGCCAAGGTGGAGGCTAGAACCTATATTGAAAC 1571
QY 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsn 450
DB 1572 TATGGCCAGATGATGTGGCTTGGAAAACTGTATATATGATGCCATACATTTCGAAT 1631
QY 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
DB 1632 GAAAGATATTAGAACTAGCGAAACTGGACTTCAATAGGTGAGTCTATACACCAACA 1691
QY 471 GluLeuLysGlyLeuGluArgTTPValValGluAsnLysLeuAspGlnLeuLysPheAla 490
DB 1692 GAGCTTCAAGATCTTCCGAGGTGGTGAATCATCCGGTTTCCAGGATCTGAATTTCACT 1751
QY 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
DB 1752 CGTGAGCGTGTGACGGAAATATATTTCTCACCGGCATCTTATCTTTGAGCCCGAGTTT 1811
QY 511 SerAspAlaArgIleSerTTPAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
DB 1812 TCTAAGTGCAGAGAGGTTTATACAAAACCTTCCAAATTTCACTGTTATTTAGATGATCTT 1871
QY 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyr 550
DB 1872 TATGACCCCATGATCTTTAGACGATCTTAAGTTGTTCCAGAGATCAGTCAAAAGATGG 1931
QY 551 AsnValAspValAspLysAspCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
DB 1932 GATCTATCACTA---GTGGACCAAAATGCCCAAAATGAAATATGTTTTGTGGTTTC 1988
QY 571 LysAspAlaIleCysTTPIleGlyAspGluAlaPheLysTTPGlnAlaArgAspValThr 590
DB 1989 TACAAATCTTTTAAATGATATAGCAAAAGAGGACGTGAGAGGCAAGGCGCGATGCTA 2048
QY 591 SerHisValIleGlnThrTTPLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyr 610
DB 2049 GGCTACATCAAAATGTTTGGAAAGTCCCACTTGAAGCTTACACGAAGAGAGCAGATGG 2108
QY 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
DB 2109 TCTGAAGCTAAATATGTGCCATCTTCAATGAATACATAGAGATGCGAGTGTCTCAATA 2168

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US-10-041-018-383 (1-784) x US-09-895-752-55 (1-2861)

Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 CTTTCCTCTCTACATTGGTGGAAACGAGAATTTCTCCAGGATTTTGGAGGATGATCTT 296
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleIleAsp 43
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 ATCGATTCTCTTAACGTCATCTCAAGAGTTGCAGCATCAGCAGGAAGCGT---ATCGAG 353
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 ACATTAATATCCGAGATTAAAGATATGTTTAGATGTATGGGCTATGCGCAAAACGAATCCC 413
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 414 TCTGCATATGACACTGCTTGGGTAGCAAGAGATTCCAGCAGTTCATGGCTCTGACAAACCC 473
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 474 CACTTTCCTGAGACGGTGTGAATGGAATCTTCAAAATCAGTTGAAGATGGTCTTGGGGT 533
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 534 -----GAAAGGATTCTACTTCTTGGCATATGACAGAAATACTTGGGTACA 575
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 576 CTTGCAATGATATTATACCCCTTACCCTCTGCGGTACTGGGGAGACACAGTACAGAAGGT 635
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
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Db	636	ATTGCAATCTTCAGGACACAAAGCTGGNAAGATCGGAAGATCGAAGCTGTAGTCATAGTCAAGGCCA	695
Qy	160	IlleGlyPheAspIlellePheProGlyLeuLeuGluTyAlaIleAsnLeuAspIleAsn	179
Db	696	AGTGGATTTGAAATAGTATTTCTCGAATCTAAAGGAAGCTAAAATCTTTAGGCTTTGGAT	755
Qy	180	LeuLeuSerIysGlnThrAspPheSerLeuMetLeuHisIysArgGluLeuGluGlnLys	199
Db	756	CTGCCTACGATTGGCAATTCCTGAAACAAATCATCGAAAAGCGGAGGCTAAAGCTTAA	815
Qy	200	ArgCysHisSerAsn-----GluMetAspGlyTyrlleuAlaTyrlleSerGluGly	216
Db	816	AGGATTCCTCCACTGATGTCTCTATGCGCTTCCAAACACGTTATTGTATTCTTTGGAAAGGT	875
Qy	217	LeuGlyAsnLeuTyrlAspTyrAsnMetValIysLysTyrlGlnMetIysAsnGlySerVal	236
Db	876	TTACAAGAAATAGTAGACTGGCAGAAAAAATAATGAAACTTCAATCCAAGGATGTCATCATTT	935
Qy	237	PheAsnSerProSerAlaThrAlaAlaIlePheIleAsnHisGlnAsnProGlyCysLeu	256
Db	936	CTACGCTCTCCGGCATCTACAGCGCTGTATTATGCTGTACAGGGAACAAAAAGTGCCTTG	995
Qy	257	AsnTyrlleuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrlProHis	276
Db	996	GATTTCTTGAACCTTTTGCTTTGAAGAAATTCGGAACCATGTGCCTTGTCTACTATCCGCTT	1055
Qy	277	AspIleuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHisHis	296
Db	1056	GATCTATTGAAAGCTTTGTGGCGGTTGTATACAGTTGAGCGGCTAGTATCTCGATCGTCAT	1115
Qy	297	PheArgValGluIleLysAsnValLeuAspGluThrTyrlArgCysTyrlValGluArgAsp	316

Qy	317	-----GluGlnIlePheMetAspValvalThrCysAlaLeuAlaPheArg	331
Db	1176	ATTGGATGGCGAGAGAGAATCTGTTCGTGATATTGATGATACAGCATGGCGGCTTCGA	1235
Qy	332	LeuLeuArgIleAsnGlyTyrGluValserProAspProLeuAlaGluIleThrAsnGlu	351

Db 1236 ATCTTGAGATTACATGATCAATGTATCTCAGATGTTTTTAAAAACATTTAGAGATGAG 1295
Qy 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
Db 1296 -----AATGGGAGTCTTTTGGTCTTGGTCAAAACACAGAGAGAGTTACAGAC 1346
Qy 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
Db 1347 ATGTTAAACGTCATCGTCTGTTTACATGTTTCATTT-----CCGGGAGAA 1391
Qy 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
Db 1392 ACCATCATGGAAGAACCAAACTCTGTACCCAAAGGTATCTGAGGAATGCTCTGGAAT 1451
Qy 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1452 GTGATGCCCTTGACAAATGGGCTTTTAAAGAAATATTCCGGGAGAGGTAGATGCA 1511
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1512 CTCATATATCCCTGGCATAGATGATGCCAAGGTGGAGCTAGAGCTATATGAAAC 1571
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrThrTyrHisSerSerAsnIleSerAsn 450
Db 1572 TATGGGCCAGATGATGTGGCTTGGAATAAAGTGTATATATATATGATGCCATACATTTGCAAT 1631
Qy 451 ThrAspTyrIleuArgIleAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1632 GAAAGATATTAGAACTAGCGAACTGGACTTCAATAAGGTGCAGTCTATACACCAACA 1691
Qy 471 GluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1692 GAGCTTCAAGATCTTCAAGGTGGTGAATATCATCCGGTTTCACGGATCTGAATTTCACT 1751
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1752 CGTGAGCGTGTGCGGAAATATATTTCTCCCGGCATCCTTTATCTTTTGAGCCGAGTTT 1811
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
Db 1812 TCTAAGTGCAGAGAGGTTTATACAAAACCTTCCAATTTCACTGTTATTTAGATGATCTT 1871
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyr 550
Db 1872 TATGACCCCATGATCTTTAGAGATCTTAAGTTGTTCAGAGATCAGTCAAAAGATGG 1931
Qy 551 AsnValAspValAspLysAspCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1932 GATCTATCACTA--GTGGACCAATGCCACAAATGAAATATATGTTTGTGGGTTTC 1988
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1989 TACAATATCTTTAATGATATAGCAAAAGAGAGCGTGAGAGCAAGCGCGATGTGCTA 2048
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyr 610
Db 2049 GGCATACATCAAAATGTTTGAAGTCCAACTTGAACCTTACAGCAAGAGAGCAATGG 2108
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 2109 TCTGAAGCTAAATATGTGCCATCTTCAATGAATACATACAGAAATGCGAGTGTCAATA 2168
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650
Db 2169 GCATTGGGAACAGTCGCTCTCTCATTAAGTGTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTTCCAAAATGATGCGAATCTAGATTTCTTCAATCTATGGGCTTAACAGGCGGT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 2289 TTGGTGNATGACCAACCAAACTTATCAGGAGAGAGGTCAGGTTGAGGTG--GCTTCT 2345

Qy 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
Db 2346 GCCATACAATGTTATATGAAGGACCATCTCTAAATCTCTGAAGAAAGCTCTACACAT 2405
Qy 709 MetMetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db 2406 GTCTATAGTGTCTATGGAATAATGCCCTCGAAGAGTTGAATAGG-----GAGTTTGTG 2456
Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsn 748
Db 2457 AATAACAAATATACCGGATATTTTACAAAGAGCTGTTTTCGAAACTGCAAGAAATATCA 2516
Qy 749 PhePheTyrAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
Db 2517 CTCTTTTATATGCAAGGGATGTTTGACACTATCATCATATATGGAATTTAAGACAT 2576
Qy 766 ValLysAspIleIleTyrAsnProLeu 774
Db 2577 GTCAAAAATTCCTCTTCCAAACCATTT 2603

RESULT 11

US-09-903-012B-55
; Sequence 55, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-903-012B-55

Alignment Scores:
Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17

US-10-041-018-383 (1-784) x US-09-903-012B-55 (1-2861)

Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
Db 237 CTTTCTCTCTCATTTGTTGAACGAGAAATTTCTCCAGGATTTTGGAAAGGATGATCTT 296
Qy 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
Db 297 ATCGATTCTTCAACGTCATCTCACAAGTTGCGATCAGACGAGAACGCT---ATCGAG 353
Qy 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluIleSerVal 60
Db 354 ACATTATATCCGAGATTAAAGATATGTTTAGATGTTGGCTATGCGGAACGAATCCC 413


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Db 1632 GAAAAGTATTAGAACTACGAACTGGAGCTTCATTAAGTGCAGTCTATACACCAACA 1691
Qy 471 GluLeuLysGlyLeuGluArgTrpValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1692 GAGCTTCAAGATCTTCCGAAGTGGTGGAAATCATCCGGTTTCACGGATCTGAATTTCACT 1751
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1752 COTGAGCGGTGACCGAAATATATTTCTCACGGCATCTTTATCTTTGAGCCCGAGTTT 1811
Qy 511 SerAspAlaArgIleSerTrpAlaLysAsnGlyIleLeuThrThrValValAspAspPhe 530
Db 1812 TCTAAGTCAGAGAGGTTTATACAAAACCTTCCAATTTCACTGTATTATTAGATGATCTT 1871
Qy 531 PheAspIleGlyGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTrp 550
Db 1872 TATGACGCCCATGATCTTTAGACGATCTTAAGTTGTTCCACAGATCAGTCAAAAGATGG 1931
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1932 GATCTATCTACTA---GTGACCAAAATGCCACAAATGAAATATGTTTGTGGTTTC 1988
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTrpGlnAlaArgAspValThr 590
Db 1989 TACATACTTTTAATCATATAGCAAAAGAGACGTGAGAGGCNAGGGCGCATGTGCTA 2048
Qy 591 SerHisValIleGlnThrTrpLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTrp 610
Db 2049 GGTACATTTCAAAATGTTTGGAAAGTCCAACTTGAAGCTTACACGAAAGACGAGAATGG 2108
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 2109 TCTGAAGCTTAAATATGTGCGCATCTCTCAATGAATACATAGAGAAATGCGAGTGTGCA 2168
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650
Db 2169 GCATTTGGGAACAGTCTTCTCATAGTCTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTCTCCAAATATGATCGCAATCTAGATTTCTTCAACTCATGGCTTAACAGGCGT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 2289 TTGGTGAATGACACCAAACTTATCAGGCAGAGAGGTCAAGGTGAGGTG---GCTTCT 2345
Qy 690 AlaLeuHisSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
Db 2346 GCCATACATGTTATATGAAGGCCATCTTAAATCTCTGAAGAGAAGCTCTACACAT 2405
Qy 709 MetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db 2406 GTCTATAGTGTATGGAATGCCCTCGAAGAGTTGAATAGG-----GAGTTTGTG 2456
Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsn 748
Db 2457 AATAACAAATACCGGATATTTACAAAGACGTGTTTGTGAACTCCAAAGATAATGCAA 2516
Qy 749 PhePheTyrAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
Db 2517 CTCCTTTATATGCAAGGGATGTTTGGACATCATCATGATATGGAATTTAAGAGCAT 2576
Qy 766 ValLysAspIleIleTyrAsnProLeu 774
Db 2577 GTCAAAATTCCTCTCTCCAAACCGATT 2603
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RESULT 13

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US-09-893-820-55
; Sequence 55, Application US/09893820
; Patent No. 6890752
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 68907521, Joseph P.
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; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-893-820-55
```

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Alignment Scores:
Pred. No.: 2,89e-110 Length: 2861
Score: 1062.50 Matches: 261
Percent Similarity: 50.6% Conservative: 148
Best Local Similarity: 32.3% Mismatches: 339
Query Match: 25.8% Indels: 61
DB: 3 Gaps: 17
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US-10-041-018-383 (1-784) x US-09-893-820-55 (1-2861)

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Qy 7 IleAlaSerProLeuLeuThrLysSerAsnArgProAlaAlaLeu-----SerAla 23
Db 237 CTTCTTCTCTACATTTGGTGAACGAGAAATTTCTCCAGGATTTTGGAGGATGATCTT 296
Qy 24 IleHisThrAlaSerThrSerHisGlyGlyGlnThrAsnProThrAsnLeuIleAsp 43
Db 297 ATCGATCTCTAACGTCATCTCACAAAGTTGCAGCATCAGACGAGAACGCT---ATCGAG 353
Qy 44 ThrThrLysGluArgIleGlnLysGlnPheLysAsnVal-----GluLeuSerVal 60
Db 354 ACATTAATATCCGAGATTAAAGAAATATGTTAGATGTATGGGCTATGGCGAAACGAATCCC 413
Qy 61 SerSerTyrAspThrAlaTrpValAlaMetValProSerProAsnSerProLysSerPro 80
Db 414 TCTGCATATGACACTGCTTTGGGTAGCAGGATTCAGCAGGTTGCGTCTGCACAAACCT 473
Qy 81 CysPheProGluCysLeuAsnTrpLeuIleAsnAsnGlnLeuAsnAspGlySerTrpGly 100
Db 474 CACTTTCCTGACAGCGTTGAATGGATTCTTCAAAATCAGTTGAAAGATGGTCTTGGGT 533
Qy 101 LeuValAsnHisThrHisAsnHisAsnHisProLeuLeuLysAspSerLeuSerSerThr 120
Db 534 -----GAAGGATTCTACTTCTTGGCATATGACAGAATATCTGGCTACA 575
Qy 121 LeuAlaCysIleValAlaLeuLysArgTrpAsnValGlyGluAspGlnIleAsnLysGly 140
Db 576 CTTGCATGTATTATTATCCCTTACCTCTGGCGTACTTGGGGGAGACACAAGTACAGAAAGGT 635
Qy 141 LeuSerPheIleGluSerAsnLeuAlaSerAlaThrGluLysSerGlnPro---SerPro 159
Db 636 ATTGAATCTTCAGGACACAAAGTGGAAAGATGGAAGCTCATAGTCATAGGCCCA 695
Qy 160 IleGlyPheAspIleIlePheProGlyLeuLeuGluTyrAlaLysAsnLeuAspIleAsn 179
Db 696 AGTGGATTGAAATAGTATTCTCTGCAATGCTAAAGGAAGCTAAAATCTTAGGCTTGGAT 755
Qy 180 LeuLeuSerLysGlnThrAspPheSerLeuMetLeuHisArgGluLeuGluGlnLys 199
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Db 756 CTGCCTTACGATTGTCCTGAAACAAATCATCGAAAGCGGAGGCTAAGCTTTAAA 815
Qy ArgCysHisSerAsn-----GluMetAspGlyTyrLeuAlaTyrIleSerGluGly 216
Db 816 AGGATTCCTCCATGCTCTCTATGCTCCCAACACAGCTTATTTGTTGGAAGGT 875
Qy LeuGlyAsnLeuTyrAspTyrAsnMetValLysLysTyrGlnMetLysAsnGlySerVal 236
Db 876 TTACAGAAATAGTAGCTGGCAGAAATTAATGAACTTCATCCAGGATGATCATTT 935
Qy PheAsnSerProSerAlaThrAlaAlaPheIleAsnHisGlnAsnProGlyCysLeu 256
Db 936 CTCAGCTCTCCGCATCTACAGCGCTGTATTATCGGTACAGGACAAACAAAGTGTG 995
Qy AsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsnAlaValProThrValTyrProHis 276
Db 996 GATTTCTTGAACCTTGTCTTGAAGAAATTCGGAACCATGCTTGTCTCATATCGCTT 1055
Qy AspLeuPheIleArgLeuSerMetValAspThrIleGluArgLeuGlyIleSerHis 296
Db 1056 GATCTATTTCAGCTTTGCTGGCGGTGATACAGTTGAGCGGTAGTATCGATCGTCAT 1115
Qy PheArgValGluIleLysAsnValLeuAspGluThrTyrArgCysTyrValGluArgAsp 316
Db 1116 TTCAAGAGGAGATCAAGGAAGCATGATGATTGTTTACAGCCATTGGGACGAAGAGGC 1175
Qy 317 -----GluGlnIlePheMetAspValValThrCysAlaLeuAlaPheArg 331
Db 1176 ATTTGGATGGCGAGAGAGATCTGTTCTCTGATATGATGATACAGCCATGGCGCTTGA 1235
Qy LeuLeuArgIleAsnGlyTyrGluValSerProAspProLeuAlaGluIleThrAsnGlu 351
Db 1236 ATCTTGAGATTACATGATACAATGATCTCTCAGATGTTTAAAAACATTTAGAGATGAG 1295
Qy 352 LeuAlaLeuLysAspGluTyrAlaAla----- 360
Db 1296 -----AATGGGAGTTCTTTTGTCTTCTGGTCAACACACAGAGAGGATTACAGAC 1346
Qy 361 ---LeuGluThrTyrHisAlaSerHisIleLeuTyrGlnGluAspLeuSerSerGlyLys 379
Db 1347 ATCTTAAACGTCATCGTTTGCATGTTTCAATTT-----CCGGGAGAA 1391
Qy 380 GlnIleLeuLysSerAla-----AspPheLeuLysGlu 390
Db 1392 ACATATGAGAGAGCAAACTCTGTACGAAAGGTATCTGAGGAATGCTCTGGAAT 1451
Qy 391 IleIleSerThrAspSerAsnArgLeuSerLysLeuIleHisLysGluValGluAsnAla 410
Db 1452 GTGGATGCTTTGACAAATGGGCTTTTAAAGAAATATTCCGGGAGAGGTAGATGCA 1511
Qy 411 LeuLysPheProIleAsnThrGlyLeuGluArgIleAsnThrArgArgAsnIleGlnLeu 430
Db 1512 CTCAAATATCCCTGGCATAGATGATGCCAAGGTGAGGCTAGAGCTATATTGAAAC 1571
Qy 431 TyrAsnValAspAsnThrArgIleLeuLysThrTyrHisSerSerAsnIleSerAsn 450
Db 1572 TATGGGCCGATGATGTGCTTGGAAACCTGTATATATGATGATGATGATGATGAT 1631
Qy 451 ThrAspTyrLeuArgLeuAlaValGluAspPheTyrThrCysGlnSerIleTyrArgGlu 470
Db 1632 GAAAGATTTTAGAATAGGAACTGAGCTTCAATAGGTGAGCTATACACAAACA 1691
Qy 471 GluLeuLysGlyLeuGluArgTyrValValGluAsnLysLeuAspGlnLeuLysPheAla 490
Db 1692 GAGCTTCAAGATCTTCGAGGTGGTGAATATCATCCGTTTACGGATCTGAAATTTCACT 1751
Qy 491 ArgGlnLysThrAlaTyrCysTyrPheSerValAlaAlaThrLeuSerSerProGluLeu 510
Db 1752 CGTGAACGCTGAGCGGAATATATTCTTCACCGGCATCTCTTATCTTTGAGCCGAGTT 1811
Qy 511 SerAspAlaArgIleSerTyrAlaLysAsnGlyIleLeuThrThrValValAspPhe 530

Db 1812 TCTAAGTCGACAGAGGTTTATACAAAACTTCCAAATTTCACTGTATTATTTAGATGATCTT 1871
Qy 531 PheAspIleGlyThrIleAspGluLeuThrAsnLeuIleGlnCysValGluLysTyr 550
Db 1872 TATGACGCCCATGATCTTTAGACGATCTTAAGTTGTTCAAGATCAGTCAAAAGATGG 1931
Qy 551 AsnValAspValAspLysAspCysCysSerGluHisValArgIleLeuPheLeuAlaLeu 570
Db 1932 GATCTATCACTA---GTGGACCAATGCCCAACAATGAATATATGTTTGTGGGTTT 1988
Qy 571 LysAspAlaIleCysTrpIleGlyAspGluAlaPheLysTyrGlnAlaArgAspValThr 590
Db 1989 TACAATATCTTTAATGATATAGCAAAAGAGGAGCGTACAGAGGCAAGGCGCATGTCTA 2048
Qy 591 SerHisValIleGlnThrTyrLeuGluLeuMetAsnSerMetLeuArgGluAlaIleTyr 610
Db 2049 GGCTACATCAAAATGTTTGGAAAGTCCAACTTGAAGCTTACAGCAAGAAAGCAATGG 2108
Qy 611 ThrArgAspAlaTyrValProThrLeuAsnGluTyrMetGluAsnAlaTyrValSerPhe 630
Db 2109 TCTGAGCTAAATATGTCATCTTCAATGATATACATAGATGCGAGTGTGTCAATA 2168
Qy 631 AlaLeuGlyProIleValLysProAlaIleTyrPheValGlyProLysLeuSerGluGlu 650
Db 2169 GCATTTGGGAACAGCTCTCTCATTTAGTCTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTCTCAAAATGATCGCAATCTAGATTTTCTCACTCATGCGCTTTAACAGGCGCT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluLysLeuAsnAlaVal 689
Db 2289 TTGCTGAATGACACCAAACTTATCAGGACGAGAGAGGTCAGGTGAGGTG---GCTTCT 2345
Qy 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
Db 2346 GCCATACAATGTTTATGAAGGACCATCTTAAATCTCTGAAGAAGAGCTTACAACAT 2405
Qy 709 MetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db 2406 GTCTATAGTGTCTATGAGAAATGCCCTCGAAGAGTTGAATAGG-----GAGTTTGTG 2456
Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTyrAsnMetCysHisValLeuAsn 748
Db 2457 AATAACAATAACCGATATTTACAAAAGAGCTGTTTTTCAAACTGCAAGAATAATGCAA 2516
Qy 749 PhePheTyrAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
Db 2517 CTCTTTTATATGCAAGGGATGTTTGACACTATCATCATGATATGAAATTTAAAGAGCAT 2576
Qy 766 ValLysAspIleIleTyrAsnProLeu 774
Db 2577 GTCAAAATTTGCTCTCTTCCAAACGAGTT 2603

RESULT 14

US-10-041-007-3
; Sequence 3, Application US/10041007
; Patent No. 6946283
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis

Db 2169 GCATTGGGAACAGTCGTTCTCATAGTCCTCTTTTCACTGGGAGGTTCTTACAGATGAA 2228
Qy 651 IleValGluSerSerGluTyrHisAsnLeuPhe---LysLeuMetSerThrGlnGlyArg 669
Db 2229 GTACTCTCCAAATGATCGGAATCTAGATTTCTTCACTCATGGCTTAAACAGGCGT 2288
Qy 670 LeuLeuAsnAspIleHisSerPheLysArgGluPheLysGluGlyLysLeuAsnAlaVal 689
Db 2289 TTGTGTAATGACACCAAACTTATCAGCGCAGAGAGGTCAAGTGTAGGTG---GCTTCT 2345
Qy 690 AlaLeuHisLeuSerAsnGlyGluSerGlyLysVal---GluGluGluValValGluGlu 708
Db 2346 GCCATCAATGTTATATGAAGGACCATCTCTAAATCTCTGAAGAAGAGCTCTACACAT 2405
Qy 709 MetMetMetIleLysAsnLysArgLysGluLeuMetLysLeuIlePheGluGluAsn 728
Db 2406 GTCTATAGTGTATGGAATATGCCCTCGAAGAGTTGAATAGG-----GAGTTGTG 2456
Qy 729 GlySerIleValProArgAlaCysLysAspAlaPheTrpAsnMetCysHisValLeuAsn 748
Db 2457 AATAACAAATACCGGATATTTACAAAGAGCTGTTTGAAGCTGCAAGAATAATGCAA 2516
Qy 749 PhePheTyrAlaAsnAspAspGlyPheThr-----GlyAsnThrIleLeuAspThr 765
Db 2517 CTCTTTATATGCAAGGGGATGGTTTGACACTATCATATGATATGGAATTTAAAGAGCAT 2576
Qy 766 ValLysAspIleIleTyrAsnProLeu 774
Db 2577 GTCAAAATATGCTCTCTTCAACACGATT 2603

RESULT 15

US-10-041-007-38

; Sequence 38, Application US/10041007

; Patent No. 6946283

; GENERAL INFORMATION:

; APPLICANT: Matsuda, Seiichi P.T.

; APPLICANT: Schepmann, Hala G

; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

; FILE REFERENCE: P02081US1

; CURRENT APPLICATION NUMBER: US/10/041,007

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: US 60/259,881

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 38

; LENGTH: 2241

; TYPE: DNA

; ORGANISM: Ginkgo biloba

US-10-041-007-38

Alignment Scores:

Pred. No.:	1,78e-109	Length:	2241
Score:	1054.00	Matches:	253
Percent Similarity:	51.2%	Conservative:	145
Best Local Similarity:	32.6%	Mismatches:	306
Query Match:	25.6%	Indels:	74
DB:	3	Gaps:	13

US-10-041-018-383 (1-784) x US-10-041-007-38 (1-2241)

Qy 33 GlyGlnThrAsnProThrAsnLeuIleAspThrThrLysGluArgIleGlnLysGln 52
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Qy 53 PheLysAsnValGluIleSerValSerTyrAspThrAlaTrpValAlaMetValPro 72
Db 37 -----TCGTGATATGATACAGCTTGGGTGGCAAGAAATTCG 72
Qy 73 SerProAsnSerProLysSerProCysPheProGluCysLeuAsnTrpLeuIleAsnAsn 92
Db 73 TCAATTGACGGCTCTGTTGGTGCACCCCAATTTCCCAACAGCTTCAATGGATTCTGAACAA 132

Qy 93 GlnLeuAsnAspGlySerTrpGlyLeuValAsnHisThrHisAsnHisAsnHisProLeu 112
Db 133 CAACTGCCAGATGGCTCGTGGGT-----GAGGAGTCATTTTTCTG 174
Qy 113 LeuLysAspSerLeuSerSerThrLeuAlaCysIleValAlaLeuLysArgTrpAsnVal 132
Db 175 GCCTATGACAGAGATTTTAAACACTCTCGCTGCTCTCTCACTCTCAAAATATGGAATAAG 234
Qy 133 GlyGluAspGlnIleAsnLysGlyLeuSerPheIleGluSerAsnLeuAlaSer---Ala 151
Db 235 GGCACATTCAGTCAGAAAGGGTTGAGTTTGTGAGAAAAACACATGGAGAAATGAAG 294
Qy 152 ThrGluLysSerGlnProSerProIleGlyPheAspIleIlePheProGlyLeuLeuGlu 171
Db 295 GACGAAGCTGACAATCACAGGCCAAGTGGATTGAGGTCTGTTCTCTGCAATGTAGAT 354
Qy 172 TyrAlaLysAsnLeuAspIleAsnLeuSerLysGlnThrAspPheSerLeuMetLeu 191
Db 355 GAAGCAAAAGCTTGGGATTGGATCTCTTATCACCTCCCTTTCATCTCCCAATCCAC 414
Qy 192 HisLysArgGluLeuGlnLysArgCysHisSerAsnGluMetAspGlyTyr----- 209
Db 415 CAAAAGCCGAGAAAAGCTTCAAAAGATTTCCCTCAATGTTCTTCAATACCATCAGACG 474
Qy 210 ---LeuAlaTyrIleSerGluGlyLeuGlyAsnLeuTyrAspTrpAsnMetValLysLys 228
Db 475 GCGTTGCTCTACTCTCTGGAGGGTTTGCAGAGTGTGTGGACTGGCAAGAGATCACAAAT 534
Qy 229 TyrGlnMetLysAsnGlySerValPheAsnSerProSerAlaThrAlaAlaPheIle 248
Db 535 CTTCAATCAAGAGACGGATCAATTTTAAAGCTCCCTGCACTACTGCTGTGCTTCTCATG 594
Qy 249 AsnHisGlnAsnProGlyCysLeuAsnTyrLeuAsnSerLeuLeuAspLysPheGlyAsn 268
Db 595 CACACTCAAAACAAAGCATGCTCCACTTCTCACTGCTGCTCAGCAATTTGGCGAC 654
Qy 269 AlaValProThrValTyrProHisAspLeuPheIleArgLeuSerMetValAspThrIle 288
Db 655 TACGTTCTTGCCATTACCACCTTGATCTATTTGAACGCTCTGGGCTGTCGATACAGTT 714
Qy 289 GluArgLeuGlyIleSerHisPheArgValGluIleLysAsnValLeuAspGluThr 308
Db 715 GAACGCTTGGGAATCGATCGCTATTTCAAGAAAGAAATCAAGAAATCTCTGGATTACGTT 774
Qy 309 TyrArgCysTrp---ValGluArgAspGlu-----GlnIlePheMetAsp 322
Db 775 TATAGTACTGGGACCCGAGAGAGCGGTGGAGTGGCAAGATGCAATCTCTATCTCTGAT 834
Qy 323 ValValThrCysAlaLeuAlaPheArgLeuLeuArgIleAsnGlyTyrGluValSerPro 342
Db 835 GTCGATGACACTGCCATGGGTCTTAGAATCTTGAGACTTCATGATACATATGATCTTCA 894
Qy 343 AspProLeuAlaGluIleThrAsnGlu----- 351
Db 895 GATGTTCTGAGAAATTTCAAGACGAGAAAGGAGACTTCTTTTGTCTTGGCGGTCAAAACG 954
Qy 352 ---LeuAlaLeuLysAspGluTyrAlaAlaLeuGluThrTyrHisAlaSerHisIleLeu 370
Db 955 CAAATTGGTGTGACCGCAAT-----CTTAACCTTTATAGATGTTTCAAGATATGT 1005
Qy 371 TyrGlnGluAspLeuSerSerGlyLysGlnIleLysSerAla----- 385
Db 1006 TTT-----CCGGGAGAAAGATAATGGAAGACCTAAGACCTTCACTTCA 1050
Qy 386 -----AspPheLysGluIleIleSerThrAspSerAsnArgLeuSerLys 401
Db 1051 AATCATCTCCAAATGCTCTTGCCAAAAACAAGCATTTTGAATGAGTGGGTGCTCAAGAG 1110
Qy 402 LeuIleHisLysGluValGluAsnAlaLeuLysPheProIleAsnThrGlyLeuGluArg 421
Db 1111 GATCTTCTGGAGAGTGGAGTATGCTATATAAGATATCCGGTGGCATAGAGATGCCAAGA 1170
Qy 422 IleAsnThrArgAsnIleGlnLeuTyrAsnValAspAsnThrArgIleLeuLysThr 441

Job time : 437.242 secs

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Db      1171  TTGGAGCGCAAGATTACATAGACCAATTGGATCAAATGATCTCGGCTGGGGAAGACT 1230
Qy      442  ThrTyrHisSerSerAsnIleSerAsnThrAspTyrLeuArgLeuAlaValGluAspPhe 461
Db      1231  GTGTATAAGATGCTATATGTGACCAACGAAATAATTGGAGCTGGCCAAATTGGACTTC 1290
Qy      462  TyrThrCysGlnSerIleTyrArgGluGluLeuLeuGlyLeuGluArgTrpValValGlu 481
Db      1291  AATATGTCGCGAGCCTTACACCAAAAGGAGACTCAACACATTGTGCAGCTGGTGGAGAA 1350
Qy      482  AsnLysLeuAspGlnLysPheAlaArgGlnLysThrAlaTyrCysTyrPheSerVal 501
Db      1351  TCGGGATTCAATGATCTTACATTCACCCGCGAGCCCTGTGGAAATGATTTCTCAGTG 1410
Qy      502  AlaAlaThrLeuSerSerProGluLeuSerAspAlaArgIleSerTrpAlaLysAsnGly 521
Db      1411  GCGGTTAGTATGTTTTCAGCCAGAAATTCGCTTGTGAGAATTGCCATGCCAAGACTTCT 1470
Qy      522  IleLeuThrThrValValAspAspPhePheAspIleGlyGlyThrIleAspGluLeuThr 541
Db      1471  TGCCTCGCAGTTATTCTAGACGATCTTACGACCCACCGGATCTCTGGATGATCTTAAA 1530
Qy      542  AsnLeuIleGlnCysValGluLysTrpAsnValAspValAspLysAspCysCysSerGlu 561
Db      1531  TTGTTCTCTGAACGGTCCGAGATGGATATCTCTGTCTGGATAGCGTTCGGGATAAT 1590
Qy      562  HisValArgIleLeuPheLeuAlaLeuLysAspAlaIleCysTrpIleGlyAspGluAla 581
Db      1591  CAGTTGAAAGTTTGTCTTCCTAGGCTGTACAACACAGTGAATGGATTTGGAAAAAGATGA 1650
Qy      582  PheLysTrpGlnAlaArgAspValThrSerHisValIleGlnThrTrpLeuGluLeuMet 601
Db      1651  CTCAGGAAACAAGCCGCTGATGTCTGGGCTATCTTCGAAAAGTATGGAGGGCTTGCTC 1710
Qy      602  AsnSerMetLeuArgGluAlaIleTrpThrArgAspAlaTyrValProThrLeuAsnGlu 621
Db      1711  GCATCGTATACCAAGAACCGAATGGTCGGCAAGTAATGTGTCGCGACATTCACACGAA 1770
Qy      622  TyrMetGluAsnAlaTyrValSerPheAlaLeuGlyProIleValLysProAlaIleTyr 641
Db      1771  TATGTGAAAAATGSCAAAGTGTCATAGCACATTCGCGACAGTCGTACTAAACTCAATCTTT 1830
Qy      642  PheValGlyProLysLeuSerGluGluIleValGluSerSerGluTyrHisAsnLeuPhe 661
Db      1831  TTCACCTGGAGAAATTACTTCTCGATTATTTACAGCAAGTAGACCTTCGGTCCAAATTT 1890
Qy      662  ---LysLeuMetSerThrGlnGlyArgLeuLeuAsnAspIleHisSerPheLysArgGlu 680
Db      1891  CTGCATCTTGTGCTTTGACTGGACGACTAATCATGACACCCAGACTTACCGCCGAG 1950
Qy      681  PheLysGluGlyLysLeuAsnAlaValAlaLeuHisLeuSerAsnGlyGluSerGlyLys 700
Db      1951  AGAAACCGTGGTGAATTTGTTTCCAGCGTACAGTG-CTACATGAGGGAATAATCCGGAGTG 2009
Qy      701  -ValGluGluGluValValGluMetMetMetMetIleLysAsnLysArgLysGluLe 720
Db      2010  CACAGAGGAAGAGCTCTAAGTCATGTTATGTTATCATCATCGACCAACGCACTGAAGGAAT 2069
Qy      720  uMetLysLeuIlePheGluAsnGlySerIleValProArgAlaCysLysAspAlaPh 740
Db      2070  G---AATGGGAGTTGGCCACCCAGAGCAATGCCCATTTGTGTGTGAGAGACTGCT 2126
Qy      740  eTrpAsnMetCysHisValLeuAsnPhePheTyrAlaAsnAspAspGlyPhe-----Th 758
Db      2127  GTTCAACACTGCAAGAGTGATCGAGCTGTTTATATGTATGATACAGAGATGGCTTTGGTATCTC 2186
Qy      758  rGlyAsnThrIleLeuAspThrValLysAspIleIleTyrAsnProLeu 774
Db      2187  TGCAAAAGAGATGAAGAGCATGTGCAGCGAACTCTTTTCGATCTGTG 2235
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Search completed: February 16, 2006, 08:16:49

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:38:14 ; Search time 2019.64 Seconds
(without alignments)
2934.525 Million cell updates/sec

Title: US-10-041-018-361

Perfect score: 2792

Sequence: 1 cccactcctcttatcaac.....aaaaaaaaaaaaaaaaa 2792

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.4	1.6	662	6	US-09-925-065A-34903
2	44.2	1.6	564	6	US-09-925-065A-830598
3	44.2	1.6	684	6	US-09-925-065A-708441
4	44.2	1.6	4023	12	US-11-098-686-9790
5	44.2	1.6	1457619	12	US-11-098-686-9790
6	44	1.6	662	6	US-09-925-065A-34904
7	42.6	1.5	534	6	US-09-925-065A-589470
8	42.6	1.5	182190	12	US-11-121-086-102
9	42	1.5	3942	9	US-11-245-147-216
10	42	1.5	3949	9	US-11-072-175-2
11	41.6	1.5	610	6	US-09-925-065A-334949
12	41.4	1.5	513	6	US-09-925-065A-200626
13	41.4	1.5	534	6	US-09-925-065A-589469
14	41.4	1.5	1230	8	US-10-793-626-3257
15	41.4	1.5	1434	8	US-10-793-626-3249
16	41.4	1.5	3410	8	US-10-793-626-3505
17	41.4	1.5	3800	8	US-10-793-626-4321
18	41.4	1.5	3818	8	US-10-793-626-3367
19	41.2	1.5	1903	8	US-10-750-185-45082
20	41.2	1.5	1903	8	US-10-750-623-45082

21	41.2	1.5	2838	12	US-11-151-601-14	Sequence 14, Appl
22	40.8	1.5	620	6	US-09-925-065A-755405	Sequence 755405,
23	40.6	1.5	555	6	US-09-925-065A-635546	Sequence 635546,
24	40.6	1.5	579	6	US-09-925-065A-664090	Sequence 664090,
25	40.6	1.5	642	6	US-09-925-065A-800116	Sequence 800116,
26	40.4	1.4	616	6	US-09-925-065A-507869	Sequence 507869,
27	40.4	1.4	5152	8	US-10-240-708-74	Sequence 74, Appl
28	40	1.4	557	6	US-09-925-065A-538851	Sequence 538851,
29	39.8	1.4	906	8	US-10-750-185-42890	Sequence 42890, A
30	39.8	1.4	906	8	US-10-750-623-42890	Sequence 42890, A
31	39.8	1.4	6152	12	US-11-196-400-1	Sequence 1, Appl
32	39.8	1.4	340000	12	US-11-102-978-3	Sequence 3, Appl
33	39.6	1.4	512	6	US-09-925-065A-605433	Sequence 605433,
34	39.6	1.4	585	6	US-09-925-065A-174571	Sequence 174571,
35	39.6	1.4	595	6	US-09-925-065A-282443	Sequence 282443,
36	39.6	1.4	1791	6	US-09-925-065A-84586	Sequence 84586, A
37	39.4	1.4	548	6	US-09-925-065A-238487	Sequence 238487,
38	39.4	1.4	579	6	US-09-925-065A-664088	Sequence 664088,
39	39.4	1.4	579	6	US-09-925-065A-664091	Sequence 664091,
40	39.4	1.4	599	6	US-09-925-065A-343016	Sequence 343016,
41	39.4	1.4	599	6	US-09-925-065A-343017	Sequence 343017,
42	39.4	1.4	601	6	US-09-925-065A-310319	Sequence 310319,
43	39.4	1.4	601	6	US-09-925-065A-310320	Sequence 310320,
44	39.4	1.4	602	6	US-09-925-065A-738779	Sequence 738779,
45	39.4	1.4	602	6	US-09-925-065A-738780	Sequence 738780,

ALIGNMENTS

RESULT 1
US-09-925-065A-34903
; Sequence 34903, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34903
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34903

Query Match 1.6%; Score 44.4; DB 6; Length 662;

Best Local Similarity 51.0%; Pred. No. 9.1;

Matches 105; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 2586 GTATAATAAGGTTGTAGTTGTTATATAAAGGTAATAGGTAATCAATAGGAAGTTAAGT 2645

DB 51 GTTTCATATATTTTGTATGCGACACAAATGAAGTAGGATATCATTTAGTAGTGCATTA 110

QY 2646 TATTAGTTTTTCCCTCGTGTACACACGGTGAAGTTCTTTGTTAAAGCAGTTTATTAT 2705

DB 111 TTTTAAATAATAAACCAAGGCAAGAGATAATGTTTACAATGTAAATATAATTAAT 170

QY 2706 GTTTAGTACACACTGGTGGTTGTTGTTGTTTATTTCTCTAAGAGCGTTTCACTTTGTT 2765


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Query Match      1.6%; Score 44.2; DB 12; Length 4023;
Best Local Similarity 51.8%; Pred. No. 20;
Matches 100; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 543 ATTGTTGCATTAAGAGATGGAATGTTGGGAAGATCAATAATAAAGTCTTAAGTTT 602
Db 3073 ACTACTACACATAAAAAATACAACTTGTCTTAATAATAAGAAAACTTCTGGCTCCCTC 3132

QY 603 ATTGAGTCAAACTCTGCTTCAGCTACTGAAAAAGTCAACCACTCTCCCATTTGTTTGAC 662
Db 3133 AATAAATCTACTATGAAATACTAATAATTATAGAGCACTACAGCTCTAAATCTTAC 3192

QY 663 ATCATATTTCTGTTGCTTGTAGTATCGAAAAAATTTGGACATAAACCCTCTCTTCAAAA 722
Db 3193 ACTGTATTTACTTCTATAAATAAGTATACCCTAACTTAGAAAAACAACTCCGTTGAGCA 3252

QY 723 CAACACAGATTTTA 735
Db 3253 CAAGCAGGTATTA 3265

RESULT 5
US-11-098-686-8739/c
; Sequence 8739, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCES: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US/11/098, 686
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8739
; LENGTH: 1457619
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Query Match      1.6%; Score 44.2; DB 12; Length 1457619;
Best Local Similarity 51.8%; Pred. No. 1.6e+02;
Matches 100; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 543 ATTGTTGCATTAAGAGATGGAATGTTGGGAAGATCAATAATAAAGTCTTAAGTTT 602
Db 1107099 ACTACTACACATAAAAAATACAACTTGTCTTAATAATAAGAAAACTTCTGGCTCCCTC 1107040

QY 603 ATTGAGTCAAACTCTGCTTCAGCTACTGAAAAAGTCAACCACTCTCCCATTTGTTTGAC 662
Db 1107039 AATAAATCTACTATGAAATACTAATAATTATAGAGCACTACAGCTCTAAATCTTAC 1106980

QY 663 ATCATATTTCTGTTGCTTGTAGTATCGAAAAAATTTGGACATAAACCCTCTTCAAAA 722
Db 1106979 ACTGTATTTACTTCTATAAATAAGTATACCCTAACTTAGAAAAACAACTCCGTTGAGCA 1106920

QY 723 CAACACAGATTTTA 735
Db 1106919 CAAGCAGGTATTA 1106907

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```

RESULT 6
US-09-925-065A-34904
; Sequence 34904, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCES: Nucleotide Polymorphisms in the Human Genome

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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34904
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-34904

```

```

Query Match      1.6%; Score 44; DB 6; Length 662;
Best Local Similarity 50.5%; Pred. No. 11;
Matches 104; Conservative 1; Mismatches 101; Indels 0; Gaps 0;

QY 2586 GTATAATAAAGGTTGTAGTTGTATAATAAAGGTAATAGGTAATCAATAGAAAGCTTAAGT 2645
Db 51 GTTTCATATATTTTGTATGCGAGCAACAATGAAGTAGGATATCATATTAGTATGCCAATTA 110

QY 2646 TATTAAGTTTTTCCCTCGTGTACACACCGGTAGGTTCTTTGTTAAAGCAGTTTATTTAT 2705
Db 111 TTTTAAATAATAAAACCAAGGCAAGAGAATAATGTTACAATGTAATAATAATTAATAAT 170

QY 2706 GTTACTAGCAGACTTGGTGGTTGTTGTTGTTTATCTCTAAGAGCCTTTCATCTTTGTT 2765
Db 171 ACTGAATTGTACACTTTAAAAAATGGTTAAAAATGTTAAATTTTGTGTCATATATTTTGT 230

QY 2766 CTTAAAAAATAAAAAAATAAAAAAATAAAAAA 2791
Db 231 ACATTAATAATAATAATAATAATAATAATAA 256

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RESULT 7
US-09-925-065A-589470/c
; Sequence 589470, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCES: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589470
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589470

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Query Match      1.5%; Score 42.6; DB 6; Length 534;
Best Local Similarity 46.2%; Pred. No. 20;

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RESULT 12
US-09-925-065A-200626/c
; Sequence 200626, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

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	Query Match	1.5%;	Score 41.4;	DB 6;	Length 534;
	Best Local Similarity	46.2%;	Pred. No. 36;		
	Matches 138;	Conservative 0;	Mismatches 161;	Indels 0;	Gaps 0;
Qy	422	TGAGTCTCAATGGTTAAATTAATCAAGCTTAATGATGTTCAATGGGCTTGTGTTAA	481		
Db	414	TGATAGTATGGTTTTTAAATATTGATTATCTCACTTGTAGCACTAGATTTTTTAAA	355		
Qy	482	TCACACTCAATATCATAAATCAACCCGTTGGCTTAAAGATTCTCTATCTTCAACATTAGCATG	541		
Db	354	ACCTAGAACAAATTAATAATCTCGTAGTTAAGTAATATTTGGCTTAAATGACGGCACTGTG	295		

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:36:26 ; Search time 2408.27 Seconds
(without alignments)
9587.015 Million cell updates/sec

Title: US-10-041-018-361
Perfect score: 2792
Sequence: 1 cccactcatcctttatcaac.....aaaaaaaaaaaaaaaaaaaaa 2792

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:
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2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2792	100.0	2792	7	US-10-041-018-361
2	2582.6	92.5	3117	7	US-10-041-018-362
3	1428.6	51.2	2594	7	US-10-041-018-368
4	809.4	29.0	2638	7	US-10-041-018-367
5	782.2	28.0	2658	7	US-10-041-018-378
6	782.2	28.0	2658	7	US-10-041-018-381
7	732.4	26.2	2506	7	US-10-041-018-377
8	561.2	20.1	2554	7	US-10-041-018-3441
9	559.6	20.0	2716	8	US-10-041-018-3441
10	466	16.7	2730	8	US-10-041-018-3441
11	433.2	15.5	2086	7	US-10-041-018-17004
12	430	15.4	2364	8	US-10-041-018-17004
13	392.4	14.1	2029	7	US-10-041-018-175619
14	379.4	13.6	2223	6	US-10-041-018-175619
15	357.4	12.8	2178	8	US-10-041-018-175619
16	356.4	12.8	2070	7	US-10-041-018-175619
17	330	11.8	1559	7	US-10-041-018-375
18	315.6	11.3	3666	7	US-10-041-018-375
19	288.8	10.3	1150	7	US-10-041-018-729
20	276.8	9.9	1008	7	US-10-041-018-729
21	275	9.8	1615	7	US-10-041-018-729
22	264.8	9.5	2193	7	US-10-041-018-729
23	241.6	8.7	2313	7	US-10-041-018-729

24	239.4	8.6	929	7	US-10-041-018-361	Sequence 51115, A
25	228.4	8.2	1157	7	US-10-041-018-361	Sequence 19703, A
26	198.4	7.1	711	7	US-10-041-018-361	Sequence 72153, A
27	194.8	7.0	2861	3	US-09-895-752-55	Sequence 55, Appl
28	194.8	7.0	2861	3	US-09-887-586A-55	Sequence 55, Appl
29	194.8	7.0	2861	3	US-09-903-012-55	Sequence 55, Appl
30	194.8	7.0	2861	3	US-09-900-797-55	Sequence 55, Appl
31	194.8	7.0	2861	3	US-09-893-820-55	Sequence 55, Appl
32	194.8	7.0	2861	5	US-10-041-007-3	Sequence 3, Appli
33	194.8	7.0	2861	7	US-10-041-018-365	Sequence 365, App
34	172.8	6.2	439	7	US-10-041-018-373	Sequence 373, App
35	172	6.2	577	6	US-10-041-018-373	Sequence 491, App
36	157	5.6	839	8	US-10-041-018-373	Sequence 167282, A
37	155.4	5.6	575	7	US-10-041-018-373	Sequence 30695, A
38	153.8	5.5	2700	3	US-09-895-752-43	Sequence 43, Appl
39	153.8	5.5	2700	3	US-09-887-586A-43	Sequence 43, Appl
40	153.8	5.5	2700	3	US-09-903-012-43	Sequence 43, Appl
41	153.8	5.5	2700	3	US-09-900-797-43	Sequence 43, Appl
42	153.8	5.5	2700	3	US-09-893-820-43	Sequence 43, Appl
43	153.8	5.5	2700	7	US-10-041-018-363	Sequence 363, App
44	151.8	5.4	1441	8	US-10-041-018-363	Sequence 170921, A
45	141.4	5.1	842	8	US-10-041-018-363	Sequence 96438, A

ALIGNMENTS

RESULT 1
US-10-041-018-361
; Sequence 361, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 361
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: Stevia rebaudiana
US-10-041-018-361

Query Match	100.0%	Score 2792;	DB 7;	Length 2792;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2792;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	CCCACTCATCTTTTATCAACCAATACATCGTTCTGCCACCGGAAGACTGATAGCGACG	60	
DB	1	CCCACTCATCTTTTATCAACCAATACATCGTTCTGCCACCGGAAGACTGATAGCGACG	60	
QY	61	GACCTCAGCAGCGCTTTTATCTCTGTGGACCACTTAAACAAATTCGACCATCATCT	120	
DB	61	GACCTCAGCAGCGCTTTTATCTCTGTGGACCACTTAAACAAATTCGACCATCATCT	120	
QY	121	ACTCCGGTGGACAGTGTTCATTTTGCATTTAGTAAATCAGCAAACTAAACATCAATGAATC	180	
DB	121	ACTCCGGTGGACAGTGTTCATTTTGCATTTAGTAAATCAGCAAACTAAACATCAATGAATC	180	
QY	181	TTTCACTATGATCGCGTCCCTTTTGTAAACCAATCAATCGACCGCGGCTCTGTGACG	240	
DB	181	TTTCACTATGATCGCGTCCCTTTTGTAAACCAATCAATCGACCGCGGCTCTGTGACG	240	
QY	241	CTATTATATGATCACTCACTTTCATGATGTTGATGATGTTGATGATGATGATGATGATG	300	
DB	241	CTATTATATGATCACTCACTTTCATGATGTTGATGATGTTGATGATGATGATGATGATG	300	
QY	301	ATACACCAAGAACGATCCAAAAACAGTTTAAAAATGTAGAAATTTCTGTTCTTCAT	360	

Qy	1640	TGCTAGGCCAAAAGACCGCCTACTGTTATTTCTCTGTTGCTGCAACATTTTCTGCTCTCCCGA	1699
Db	1966	TGCTAGGCCAAAAGACCGCCTACTGTTATTTCTCTGTTGCTGCAACATTTTCTGCTCTCCCGA	2025
Qy	1700	ATTATACAGATGCGCGTATTTTCATGGGCCAAAATGGCATATTAACACAGTAGTGTGATGA	1759
Db	2026	ATTATACAGATGCGCGTATTTTCATGGGCCAAAATGGCATATTAACACAGTAGTGTGATGA	2085
Qy	1760	CTTTTTTTTGATATCGGTGGTCAATCGATGAATTTGACCAACTGATTTCAATGTCTTGAAGA	1819
Db	2086	CTTTTTTTTGATATCGGTGGTCAATCGATGAATTTGACCAACTGATTTCAATGTGTGTGAAGA	2145
Qy	1820	ATGGAATGTAGATGTCGACCAAGGATTTGTTTCAGAGCATGTTCCGATTTTATTTTATTTAGC	1879
Db	2146	ATGGAATGTAGATGTCGACCAAGGATTTGTTTCAGAGCATGTTCCGATTTTATTTTATTTAGC	2205
Qy	1880	ATTAAAAAGATGCAATCTGTTGGATGGAGATGAAGCTTTTAAATGGCAAGCGCGCGATGT	1939
Db	2206	ATTAAAAAGATGCAATCTGTTGGATGGAGATGAAGCTTTTAAATGGCAAGCGCGCGATGT	2265
Qy	1940	AACATGCGCATGTTATTTCAAACTTTGGTTGGAACTTAATGAATAGTATGTTTGAGAGNAGCTAT	1999
Db	2266	AACATGCGCATGTTATTTCAAACTTTGGTTGGAACTTAATGAATAGTATGTTTGAGAGNAGCTAT	2325
Qy	2000	ATGGACAAGAGATGCTTATGTGTCCAACATTTAAATGAATATATGAGAAAACGCTTACGTGTC	2059
Db	2326	ATGGACAAGAGATGCTTATGTGTCCAACATTTAAATGAATATATGAGAAAACGCTTACGTGTC	2385
Qy	2060	ATTGTCAATTAGGCCCGATGTCGAAGCGGCTATTTACTTTGTGGGGCCCCAAATTTATCAGA	2119
Db	2386	ATTGTCAATTAGGCCCGATGTCGAAGCGGCTATTTACTTTGTGGGGCCCCAAATTTATCAGA	2445
Qy	2120	GGAGATTGTTGAAAGCTCTGAATATCATATCTATTTTAAGCTAATGAGCAGCAGGGTCG	2179
Db	2446	GGAGATTGTTGAAAGCTCTGAATATCATATCTATTTTAAGCTAATGAGCAGCAGGGTCG	2505
Qy	2180	ACTTCTTAAACGATATCCATAGCTTCAAGAGGGAATTTTAAGGAAAGGCAAAATTTAAACCGGT	2239
Db	2506	ACTTCTTAAACGATATCCATAGCTTCAAGAGGGAATTTTAAGGAAAGGCAAAATTTAAACCGGT	2565
Qy	2240	AGCATTTGCATTTTGAGTAAACGAGAAAGTGGAAAGTGGAAAGAGAGTCTGTGAGGAGAT	2299
Db	2566	AGCATTTGCATTTTGAGTAAACGAGAAAGTGGAAAGTGGAAAGAGAGTCTGTGAGGAGAT	2625
Qy	2300	GATGATGATGATTTAAAAACAGAGGAAGAATTAATGAAATTAATTTTGTGAAGAAATGG	2359
Db	2626	GATGATGATGATTTAAAAACAGAGGAAGAATTAATGAAATTAATTTTGTGAAGAAATGG	2685
Qy	2360	TAGCATTTGTTCTAGAGCTTGTAAAGATGCATTTTGGAAATGTCGTACCGTGTGAATTT	2419
Db	2686	TAGCATTTGTTCTAGAGCTTGTAAAGATGCATTTTGGAAATGTCGTACCGTGTGAATTT	2745
Qy	2420	TTTTTACGCAAAACGATCAGGGTTTACTGGAACACCGATTTCTTGATACTGTGAAGGACAT	2479
Db	2746	TTTTTACGCAAAACGATCAGGGTTTACTGGAACACCGATTTCTTGATACTGTGAAGGACAT	2805
Qy	2480	CATTTACAAACCGTTGGTGTCTGTGAATGAAATGAAAGAAACAAAGGTAATTTGGCCTTTAA	2539
Db	2806	CATTTACAAACCGTTGGTGTCTGTGAATGAAATGAAAGAAACAAAGGTAATTTGGCCTTTAA	2865
Qy	2540	AAGATGATAATAATATCATGCTTGTGACGGGGTACTGTTGTAGTGTGTATTAATAAGGTT	2599
Db	2866	AAGATGATAATAATATCATGCTTGTGACGGGGTACTGTTGTAGTGTGTATTAATAAGGTT	2925
Qy	2600	GTAGTTCTGTAAATAAGGTAATAGGTAAATCAATAGAAAGCTTAAGTTATTAAGTTTTTCC	2659
Db	2926	GTAGTTCTGTAAATAAGGTAATAGGTAAATCAATAGAAAGCTTAAGTTATTAAGTTTTTCC	2985
Qy	2660	CTCGTGTCAACACCGGTGAGGTTCTTGTATAAGCAGTTATTTTATGTTTAGTACGACAC	2719
Db	2986	CTCGTGTCAACACCGGTGAGGTTCTTGTATAAGCAGTTATTTTATGTTTAGTACGACAC	3045

Qy	2720	TTGTGTTGTTGTTGTTGTTTATTTCTCTAAGAGGCTTTCACTTTGTTCTTTAAAAAAA	2776
Db	3046	TTGTGTTGTTGTTGTTGTTTATTTCTCTAAGAGGCTTTCACTTTGTTCTTTAATAAGAA	3102
RESULT 3			
US-10-041-018-368			
; Sequence 368, Application US/10041018			
; Publication No. US20040072323A1			
; GENERAL INFORMATION:			
; APPLICANT: Mateuda, Seiichi P.T.			
; APPLICANT: Hart, Elizabeth A.			
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism			
; FILE REFERENCE: P02080US1/10025547			
; CURRENT APPLICATION NUMBER: US/10/041,018			
; CURRENT FILING DATE: 2002-01-07			
; PRIOR APPLICATION NUMBER: US 60/259880			
; PRIOR FILING DATE: 2001-01-05			
; NUMBER OF SEQ ID NOS: 413			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 368			
; LENGTH: 2594			
; TYPE: DNA			
; ORGANISM: Lactuca sativa			
US-10-041-018-368			
Query Match 51.2%; Score 1428.6; DB 7; Length 2594;			
Best Local Similarity 75.8%; Pred. No. 0;			
Matches 1833; Conservative 0; Mismatches 529; Indels 57; Gaps 3;			
Qy	238	CAGCTATTTCATCAGCATCAACTTCATCGTGGGACAAACTAATCCACCTAAATCTGATCA	297
Db	187	CATCGGGTCTTCGTACAGCTCTTCACAGCTGGACAGGTTAATCCTACTGTCATGACCC	246
Qy	298	TTGATACAAACCAAGAACGGATCCAAAACAGTTTAAAAATGTAAGAAATTCCTGTTTCTT	357
Db	247	TTGATGTGACCAAGAACGAATCCGAAGCTGTTCAACATGTGGAAGTTTCTGTTTCTT	306
Qy	358	CATATGACACAGCATGGGTAGCAGTGGTCCCTTCTCCAACTCACCCAAATCCGCTTGTT	417
Db	307	CATATGACACAGCTTGGGTAGCATGGTCCCTTCTCCAACTCTCCAAATCCCTTGTT	366
Qy	418	TCCCTGAGTGTCTCAATTTGGTTAATTAATAATCAGCTTAAATGATGGTTTATGGGGTCTTG	477
Db	367	TCCCTGATGTCTGCACTGGTTACTGGATTAATCAGCTTGTATGATGGTTTATGGGGTCT--	424
Qy	478	TTAATCACACTCAATAATCAATAATCACCGGTGTTTAAAGATTCCTATCTTCAACATTAG	537
Db	425	-----TCTTCTCTCATCAGTCCGCCATTAATTAAGATACTCTCTCTTCAACATTAG	474
Qy	538	CATGTATTGTGCTATTAAGAAAGTGGATGTTTGGGAGAGTCAATTAATAAGAGGTCTAA	597
Db	475	CATGTGTACTTGCATTAAACCGATGGAATGTGGGAAAGACCAAAATTAACAAAGGTTTAC	534
Qy	598	GTTTTATTGAGTCAAATCTTGTCTCAGCTACTCGAAAAAGTCAACATCTCCCATTTGGTT	657
Db	535	ATTACATTGAGTCMAATTTTGCTTTCAGTCTACTGACAAATCAAGCATCTCCATTTGGTT	594
Qy	658	TTGACATCATATTTTCTGGTTTGTCTTGAGPATGCGAAAAAATTGGACATAAAACCTCCTTT	717
Db	595	TTGACATCATATTTTCTGGTGTATGCTTGAGTATGCAAAAGATTTGGATATAAAACTCCCTT	654
Qy	718	CAAAAACACAGATTTTAGTTTGATGCTACATAAGAGGGAATTTGGAGCAAAAAGATGCC	777
Db	655	TAAACCAACACATTTTGAGTGTGATGTTACATGAGAGAGAATTTGGAGCTAAGAAGATGC	714
Qy	778	ATTCABAATGAGATGGATGATCTTGCGGTATATCTCTGAAGGACTCGGTAAATTTTATATG	837
Db	715	ATTCAAAATGGAGGAAGACATCTTGGCATATATCTCAGAAAGCAATTTGGAATTTAAATG	774
Qy	838	ATTGGAAATGCGTGAAGAAATATCAGATGAAAAATGGTTCTGTTTTCAACTCAACATCAG	897
Db	775	ACTTGGACATGGTGTGTAAGAAATATCAATGAAGAAATGGTTCTCTTTTCAACTCAACCTCAG	834

Qy	267	GGTGGACAAACTAATCCCACTAATCTGTGATCATATCAACCAAGAACGGATCCAAAA	326
Db	159	GGCACAAAACTAAAACTGGAGCTTTGCGCTTTGAGAAACAAAAAGAAATAAAAAA	218
Qy	327	CAGTTTAAANAATGTAGAAAATTTCTGTCTTTCATATGACACAGCATGGGTAGCCATGGTC	386
Db	219	TTGTTCAAAAAATGTGTGAACCTTTCAATTTCTGTCATATGATCTGCATGGGTGGCAATGGTC	278
Qy	387	CTTTCTCCAAACTCACCCAAATCCCTTGTTTCCCTGAGTGTCTCAATTTGGTTAAATTAAT	446
Db	279	CTTTCTCCAAACTCTCTTAATAAACCTCTTTTCTGAGTGCAATAACTGGGTATTAGAT	338
Qy	447	AATCAGCTTAAATGATGGTTTCATGGGGTCTTGTGTTAATCACACTCATATAATACACCCG	506
Db	339	CATCAAAACCCGTATGGGTATGGGG-----CATACTCCATGACCATCAGTTG	386
Qy	507	TTGCTTTAAAGATTTCTCTATCTTTCAACATTTAGCATGTATTGTTGCAATTAATAAGATGCAAT	566
Db	387	GTGATGAAAGCCACTCTCTTTATCCACATTTAGCATGTGTCTTACTCTTTAAGCGATGGAT	446
Qy	567	GTTCGGGGAAGATCAAAATAAATAAAGTCTAAGTTTATTGAGTCAAAATCTTGCTTTCACT	626
Db	447	ATCGGTGATGATCATATGAGCAAGGCCCTTAGTTTATCAAGTCTAATAATAGCTTTCACT	506
Qy	627	ACTGAAAAAAGTCAACCATCTCCCATCTGGTTTTCACATCATATTTCTCTGGTTTCTTTGAG	686
Db	507	ACTGATGAGTAATCAACGTTCTCTCTGGGATTTTGACATAATTTTCCCTGGTATGATTTGAG	566
Qy	687	TATCGGAAAAACTTTGGACATAAACCCTCTCTTTCAAAAACAAACAGATTTTGTGTTGATGCTA	746
Db	567	TATCTTAAAGACTTTGAAATTTGAAATCTACCTTGGCATCAATGAAATGTGGATGCTTTGGTT	626
Qy	747	CATAAGAGGGAATTTGGAGCAAAAAAGAT-----GCCATTCAATGAGATGGATGGATAC	800
Db	627	CAAAAGAAAGAGTTTGGAGCTTTAGAAAGCTGCTGTAGCAACTCTGAAGGAGGAAAGCCAT	686
Qy	801	TTGCGGTATATCTCTGAAGGACTCGGTAAATTTATGATTTGGAATATGGTGAAGAAATAT	860
Db	687	TTAGCTGATGTTTCAGAAGGNAITGGAAATTTACAGAGCTGGGAAATGGTATGCGATAT	746
Qy	861	CAGATGAAAAATGTTCTGTTTTCAACTCACCATCAGCAACAGCTGCTGCTTTTCATTAAAT	920
Db	747	CAAGGGAAGAACGGATCACTGTTTAGTTCTCCATCCACCACGGCAGTGGCTTTTATGCGAC	806
Qy	921	CATCAAAATCCTGTTGTTCTTAATTTAATTTCACTTTTGGACAAGTTTGGTAAATGCA	980
Db	807	AGAAATGATGATGGCTGTTTAAATTTACCTTCGCTCAGTCTTTACAAAAGTTTCATAGTTCA	866
Qy	981	GTCCCAACAGTTTATCTCTCATGATTTATTTATCCGACTTTCTATGGTTTGACACAATTTGAA	1040
Db	867	GTTCGCCGAATATATCTCTTGATATATATGCTCGTTTACATGTTTGATAGCCTTCAA	926
Qy	1041	AGATTAGGAATTTCCACACCATTTCAGAGTGGAAATTAATAATGTTTTAGATGAACAATAC	1100
Db	927	AAACTGGGATTTGATGGCCATTTCAAAGATGAGATTAGAAGTGTATTAGATGAACAATAC	986
Qy	1101	AGATGTTGGGTGGAAAGAGATGAGCAAAATATTCATGGAGTTGTGTAAACATGTGCTTTAGCC	1160
Db	987	AGCTGTTTGGATGCAAGGGGAGGAAAAATATTCCTAGATGCTTCAACTTTGTGCAATGGCC	1046
Qy	1161	TTTTCGGTTATTAAAGGATCAATGGGTATGAGTTTCCCAGATCCATTTGGCTGAAATTAAT	1220
Db	1047	TTCCGGATGTTACGTGTGTGAAGGATATGATGTTTCTTCAGATCAATTTGACTCAATTTCTCA	1106
Qy	1221	AA-----TGAATTTAGCTTTTGAAGACGCAATATGCGAGCTCTTTGAA	1259
Db	1107	GAAGGTCTCTTTTCAAATTGCTCGGAGGACATTTAAAGACTTTTAGTGCTCACTAGAG	1166
Qy	1260	ACATATCATGCGTCACA---TATATTTATACAGAGGATTTATCTTCTGGAAAAACAATC	1316
Db	1167	TTATTTAAGGCCCTCCAGATTTATCAITTTATCCGATGAGTTTATTTCTTGGAAAAATATAAC	1226

Qy	1317	TTGAGTCAGCTGATTTTCCTCAAGAGATAAATATCACTG-----ATTCAACACAGG	1367
Db	1227	TCTTGGACTAGTCGTTTCTCGTAATCATGGAATATCTAGTGGTTCACTTCAATCTGATAGA	1286
Qy	1368	CTTTCTAAATTAATTCACAAAGAGGTGGAAATAGCTCTTAAAGTTCCCTATCAATACCGGT	1427
Db	1287	ACTGAGAGACTCGTGAAACAAGAGGCGAGTTATGCTTTCGAGTTCCCTATTAATTTCAACT	1346
Qy	1428	TTAGAACGCATAAACACTAGACGAAATATACAGCTTTTCAATGTAGACAATACAAGAAATT	1487
Db	1347	CTGGAACGCTTATCAAAATGAAGCGAGCACTGGAAAGTTACAGTGGAGACATTTGTGAGGAATT	1406
Qy	1488	CTGAAAACTACATATCACTCATCAATATATTAGTAAACATGATTAACCTAAGTTGGCTGTT	1547
Db	1407	TCAAAAACAGCATATGCTGCTTTAAATTTTGGTTCATCAAGATTTCTTTGGAACCTGTCTGTA	1466
Qy	1548	GAAGATTTCTACACCTGCCAATCTATTTATTCGTGGAAGAATTTAAAGGTCTTTGAAAGTGTG	1607
Db	1467	GAAGATTTCAATACCTGCAAGGCATACATCGCAAGAACTGAAAGAGCTTGHAAAGCTTGHAAATGTG	1526
Qy	1608	GTGGTAGAAGTAAGTTGGACCAAGCTCAAGTTTGTGTAGGCAAAAGACCGCCTACTGTTAT	1667
Db	1527	GTCAATCGAANAACAAATGGACAGATTGAAATTTGCGAGACAGAACTAGCGTACTGCTAT	1586
Qy	1668	TTCTCTGTGCTGCAACACTTTTCGTTCCCGAATATCAGATGCGGCGTATTTTCATGGGCC	1727
Db	1587	TTTTCTGCTGACGCAACCTTAACCTCTCCAGAACTTTGTGATGCGCGCTTATCATGGGCA	1646
Qy	1728	AAAAATGGGCATATTAACACAGTATGATGACTTTTGTGATATCGTGGTGAACAATCGAT	1787
Db	1647	AAAAATGGGGTACTCAACACCGGTGTGATGATTTCTTTGATGTGGAGGATCTGAAGAG	1706
Qy	1788	GAATTTGACCAACCTGATTCAAATGTTTGAANAATGGAATGTAGATGTGCAACAAGGATTTGT	1847
Db	1707	GAATTTGTAACCTTATACAAATGGTGGAAAGTGGGATGCCAGTGGGGAACCGGTTAC	1766
Qy	1848	TGTTTCAGAGCAATGTTCCGATTTTATTTTATAGCAATTAAGAATGCAATCTGTGGATGGA	1907
Db	1767	TGTTTCCAAGAGGTTTGAGATTAATTTCTTGCACCTTCATAGCACAAATTTGTGAAATPAGA	1826
Qy	1908	GATGAAGCTTTTAAATGGCAAGCCGCGATGTAACTAGCCATGTTTATTCAAACTTTGGTTG	1967
Db	1827	AAAAAAGCTTTTACTCTTGGCAAGGACCGCGTGATGAGGAATGTTATCGATATTTGGTTG	1886
Qy	1968	GAACATATGAATAGTATGTTGAGAGAAGCTATATGACCAAGAGATGCTTATGTGCCAAACA	2027
Db	1887	GCCTTGTCTGAGTCATATGAGGAAGGAAGCTGAATGTTGAAANAATGAAGTAGTGCATCA	1946
Qy	2028	TTAAATGAATATATGAAAAACGCTTACGTGTCAATTTGCAATTAGGCCGAGTTGTCAAGCCG	2087
Db	1947	TTGGATGAGTACATGAAATAATGCTATGTATCATTTGCTTTGGGACCTATAGTCTTCCA	2006
Qy	2088	GCATTTTATCTTTGTGGGGCCCAATTTATCAGAGGAGATTTGTTGAAAGCTCTGNAATCAT	2147
Db	2007	ACGCTCTACTTTGTGGACCTTAAGCTTCCAGAGGAAATTTGTTGGAATTTGTGAATACAAG	2066
Qy	2148	AATCTATTTAAGCTATATGAGCACGAGGTCGACTTCTTAAACGATATCCATAGCTTTCAAG	2207
Db	2067	AAGCTCTTTAAGCTGATGAGCACTTCGCGCGCTTCTGAAATGATACTGAACTTTTGAT	2126
Qy	2208	AGGGAATTTTAAAGGACCAATTTAAACCGCGTAGCATTTGCAATTTAGTAACGAGAAAAGT	2267
Db	2127	AGAGAGTCCAGCGAAGGGAATTTAATGCTTTGTCTCTATACATGATTAGTCCGCTGGT	2186
Qy	2268	GGGAAAGTGAAGAAGAGGTTGTGGAGGAGATGATGATGATGATTTAAAAACAAGAGAAA	2327
Db	2187	AAGCTCACCAAGAGAGGAGGCCACTGAAGCAATGAAAGAGAGATGTTGATAGGACGAGAAGA	2246
Qy	2328	GAATTAATGAATTAATTTTGAAGAAATATGGTAGCATTTGTTCTAGAGCTTCTTAAGAT	2387
Db	2247	GAACTGTGTGATATGTTTGTGAGGAGAACAGTACAA---TTCCAAGAGCTTGTAAAGAT	2303
Qy	2388	GCATTTTGGAAACATGTGTCACTGTTTGAATTTTTTTTTTATCGCAAAACGATGACGGTTTACT	2447

1856 GCATGTTCCGATTTTATTTTATAGCAATTAAGATGCAATCTGTTGGATTGGAGTGAAGC 1915
 1844 GGACGTTGAGATTGATTTTCTTGCACTGACAGCACAGTTTGTGAATAGGAGAGAGC 1903
 1916 TTTTAAATGCGAAGCGCGGATGTAACATAGCCATGTTTCAAACTTGGTTCGAACTAAT 1975
 1904 TTTAGTATGCGAAGGACGCGAGTGTATAGGAATGTTATCGATGGTGTGGTCTGCT 1963
 1976 GAATAGTATTTGAGAGAGCTATATGGAACAAGAGATGCTTATGTGCCAACATTAATGA 2035
 1964 GAAGTGATGAGAAAGGAGCTGAATGGTTCGACAAATAGGTAGTGCCTAATGGTGA 2023
 2036 ATATATGGAACCGTTAGCTGTCATTTGCAATAGGCCGATGTCAGCCGGCTATTATTA 2095
 2024 ATATATGGAACCAAGCCCATGTATCTCGCTTGGGACCTATAATCTTTCCAAATGCTCT 2083
 2096 CTTTGTGGGGCCAAATATATCAGAGAGATGTTGAAAGCTCTGAATATCATAACTATT 2155
 2084 CTTTGTGGACCTAACTCTCAGAGGAATGATGGAAGCTGTGAATACCAAGATTATA 2143
 2156 TAAGCTAATGAGCAGCGAGGCTCGACTTCTAAACGATATCCATAGCTTCAAGAGGGAATT 2215
 2144 TAAGCTGATGAGCACTGCTGGTTCGCTTAAGAAATGATATTCGATCTTACGATAGAGATG 2203
 2216 TAAGGAGGCAAAATTAACCGCGGTAGCATTTGCAATTTAGTAACGAGAAAGTGGGAAAGT 2275
 2204 CAAAGAGGGAAGCTGAATATTTCTGTCTGTGGATGATTTGATGGCGGTGTAATGTCTAC 2263
 2276 GGAAGAAGAGGTTGTGGAGGAGATGATGATGATGATTAATAAACAAGAGAAAGAAATTAAT 2335
 2264 CAAAGAGGAGGCCATTGAAGCAATTAAGGGGATTTTGAAGGGCGATGAAGAGAGCTGCT 2323
 2336 GAAATTAATTTTGAAGAAAATGGTAGCAATTTCTAGAGCTTTGTAAAGATGCAATTTTG 2395
 2324 GGGGTAGTTTTCAGAGAACTACAA--TTCCAAGAGCTTGTAAAGATTTGTTCTG 2380
 2396 GAAATGTGTACGTTGGAATTTTTCGAAACGATGACGCGGTTTACCTGGAACAC 2455
 2381 GAAATGTGTCCATTTGTGAATCTATTTTACATGGAAGATGATGGGTACACTTCAAATAG 2440
 2456 GATTTCTGATCTGTGAAGGACATCATTTTACACCGTTGGTGTG 2502
 2441 GTTATGTAACCTGTAAAGGCCATGTTTGAACAACCCATGGATCTGG 2487

RESULT 6

US-10-041-018-381
 ; Sequence 381, Application US/10041018
 ; Publication No. US20040072323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuda, Seiichi P. T.
 ; APPLICANT: Hart, Elizabeth A.
 ; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
 ; FILE REFERENCE: P02080US/10025547
 ; CURRENT APPLICATION NUMBER: US/10/041,018
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: US 60/259880
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 381
 ; LENGTH: 2658
 ; TYPE: DNA
 ; ORGANISM: Cucurbita maxima
 US-10-041-018-381

Query Match 28.0%; Score 782.2; DB 7; Length 2658;
 Best Local Similarity 61.3%; Pred. No. 4.5e-173;
 Matches 1390; Conservative 0; Mismatches 823; Indels 54; Gaps 6;
 275 AACTAATCCCACTATCTGATCATGATACACCAAGAACGATCCAAAACAGCTTTAA 334

236 AACTAAAACCTGGAGCTTTTGCACCTTTTGAAGAAACAAAAGAAATTAAGAAATTTGTTGCA 295
 335 AAATGTAGAAATTTCTGTTTCTTATATAGACACAGCATGGGTAGGCATGGTCCCTTCTCC 394
 296 CAAGGTGAACCTTTCAGTTTCTGCATATGATACTGATGGGTGGCAATGGTTCCTTCTCC 355
 395 AAACCTCAACCAATCGCCTTGTTCCTCCCTGAGTGTCTCAATTCGTTTAAATTAATAACAGCT 454
 356 AAACCTCTCTCAACCAACCTTTTCCCGAGTGTATAAACTGGGTATTAGATAGTCAACA 415
 455 TAATGATGTTTCATCGGGCTTTGTTAAATCACACTCATATCATATCAATCAACCCGTTGCTTAA 514
 416 TGCTGATGGCTCATGGGGCTTACTCCAAAC-----GATCAGTTGCTGATGAA 463
 515 AGATTTCTATCTTCAACATATAGCATGTATTGTGCAATTAATAAAGATGGAATGTTGGGGA 574
 464 GGCCAAATCTTATCTACATTAAGCATGTGTTCTTACTCTTAAGCGGTGGAATATTGGGCA 523
 575 AGATCAAAATAAATAAGGTCTAAGTTTATTCAGTCAAAATCTTGTCTCAGCTACTCAAAA 634
 524 TGATCATATGACAGAGGCCCTTGTATTTTATCAAGTCTAATATAGCTTTCAGCTACTGATGA 583
 635 AAGTCAACCATCTCCCATTTGGTTTTGACATCATATTTCTCGTGTTCGTTGAGTATCGGAA 694
 584 GAAACCAACGTTCTCCGGTGGGATTTGACATTAATTTCCCTGCAATGATTGAGTATGCTAA 643
 695 AAATTTGACATTAACCTCTTTTCAAAAACAAACAGATTTTATGTTGATGCTCATATAAGAG 754
 644 AGACTTGAATTTGAATCTACCTTGGCACCGACGAAACGTGGATGCTTGGTTCGAAAGAA 703
 755 GGAATTTGGAGCAAAA-----AGATGCCATTTCAATGAGATGAGTGGATGATCTTGGCGTA 808
 704 AGATTTGGAGCTGGAAGGCTGCAGAAAGCAACTCTGAAAGTGGAAAGCCCTATTAGCGTA 763
 809 TATCTCTGAAGGACTCGGTAAATTTATATGATTGGAATATGTTGGAAGAAATATCAGATGAA 868
 764 TGTTTCAGAGGAATTTGGAAGTTACAGGACTGGGATGTTGTCATGCAATATCAAGAGAA 823
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 824 GAATGGATCAGCTGTTTAAATTTCTCCATCCACTACGCGCAGCGGCTTTTATGCATAGAATGA 883
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 989 AGTTTATCTCATGATTTTATTTATCCGACTTTCTATGTTTGACACAAATTTGAAGATTAGG 1048
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 1064 GATGCAAGGAGAGGAAATATATTTCTTAGATGCTTCAACTGTTGCAATGGCCCTTTGCAAT 1123
 1169 ATTAAGGATCAATGGGTATGAAGTTTCCCGAGATCCATTCGCTGAAATTAATACTAA----- 1222
 1124 GTTACGTGTTGAAGGATGATGTTTCTTCAGACCCAGTTGACTCAATTTTCAGAAGATAT 1183
 1223 -----TGAATTAGCTTTTGAAGACGAATATGACGCTTCCTTGAACATATCA 1267
 1184 CTTTCCCAATTCGCTTGGAGGATATTAAAGAGACTTCGCTGCTCGCTGGAGTTATATAA 1243
 1268 TCGGTCAATATATATACCAAGAGGATTTATCTTCT---GGAAACAATCTTGAAGTC 1324
 1244 GGCCTCTCAGATTATACCGCACCCCGAGTGAATCTGTCTTGGAAATATTAACACTTTGGAC 1303
 1325 AGCTGATTTCTTCAAGAGATTAATATCCACTGATTAACAAACAGGCTTTCTAAA----- 1376
 1304 TAGTCGTTCTTGAAGCATGGATTATCTAGTATTCAGTTTGTCTGTAGTAAACCGATAG 1363

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QY 1377 -TTAATTCAAAAGAGGTGAAATGCTCTTAAGTTCCTATCAATACCGGTTTAGAACG 1435
Db 1364 TGTGTTAAACAAGAGCTGTTAATGCTCTTGAGTTCCTCTAATATGCAACTCTAGAACG 1423
QY 1436 CATAAACACTAGACGAAATATACAGCTTTTCAATGTAGACAAATACAGAAATCTGAAAC 1495
Db 1424 CCTAATAAGTAAGAGGCAATGAAAGTTACAGTGGAGACATTTGAGAGGATTTCAAAATC 1483
QY 1496 TACATATCACTCAATCAATATTAGTAACTATACCTTAAGTTCCTGCTGCTTGAAGATTT 1555
Db 1484 GCCATATGCTGCTTAAATTTTGGCCCACTCAAGATTTCTGGAACCTTGTCTAGAGGATTT 1543
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QY 1736 CATATTAACTACAGTAGTTGATGACTTTTTTGTATCGGTGGTACAAATCGATGAATTGAC 1795
Db 1724 TGTGCTCACACCGTGTGATGATTTCTATGATGTTGGAGGATCTGAAGAGGAATTTGA 1783
QY 1796 CAACCTGATTTCAATGTGTTCAAAAATGGAATGTAGATGTGCAAGAGGATTTGTTTCAGA 1855
Db 1784 TAACCTTATAGAAATGGTGAAGAGTGGATCTGATGGGGAAGTGGTTACTGTTCCAA 1843
QY 1856 GCATGTTGGAATTTATTTTATAGCAATTAAGATGCAATCTGTTGGAATGGAGATGAAC 1915
Db 1844 GGACGTTGAGATTTGATTTCTTGCACTGCACAGACAGATTTGTGAATAGGAAGAAGAGC 1903
QY 1916 TTTTAAATGCAAGCGCGATCTACTAGCCATGTTATTCAACTTTGTTGGTGAACATAAT 1975
Db 1904 TTTAGTATGCAAGGACGAGTGTATGAGGAATGTTATCGATGGTGGTGTGCTCTGCT 1963
QY 1976 GAATAGTATGTTGAGAGAACTATATGGAACAAGAGATGCTTATGTGCAACATTAATGA 2035
Db 1964 GAAGTGTAGAGAAAGAAAGCTGAATGTTGCAAAATAGAGTAGTCCATCAATGGGTGA 2023
QY 2036 ATATATGGAACCGTTACGTGCTATTTGCAATTAAGCCGATTTGTCAAGCCGGCTATTTA 2095
Db 2024 ATATATGGAACAAGCCCATGTATCATTCGCGTTGGGACCTTAAATCCTTCCAATGCTCTT 2083
QY 2096 CTTTGTGGGCCCCAAATTAATCAGAGGAGATTTGTAAGCTCTGAATATCATATCATTTAT 2155
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QY 2156 TAAGCTAATGAGCACGAGGCTGACTTCTAAACGATATCCATAGCTTCAAGAGGGAAT 2215
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QY 2216 TAAGGAAGGCAATTAACCCGGTAGCATTTGCAATTTAGTAAACGAGAAAGTGGGAAGT 2275
Db 2204 CAAAGAGGAAAGCTGAATTTCTGCTCTGCTGATTTGATGATGGCGGTAAATGTCAC 2263
QY 2276 GGAAGAAGAGGTTGTGGAGAGATGATGATGATTTAAACACAGAGGAAGAAATTAAT 2335
Db 2264 CAAAGAGAGGCCATTTGAAGCAATTAAGGGGATTTTGAAGGGCGGATTAAGAGCTGCT 2323
QY 2336 GAAATTAATTTTGAAGAAATGTTAGCAATTTCTTCTAGAGCTTGTAAAGATGCAATTTG 2395
Db 2324 GGGGTAGTTTTCAGAGAAACACTACAA---TTCCAAGAGCTTGTAGAGATTTGTTCTG 2380
QY 2396 GAACATGTGTACGTGTTGAATTTTATGCAAAACGATGACGGGTTTATCTGGAACAC 2455
Db 2381 GAAATTTGATGTCATTTGTTGATCTATTTTACATGGAAGATGATGGGTACACTTCAAAATG 2440
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QY 2456 GATTCTTGATCTGTGAAGGACATCATTTTACAACCGTGTGGTCTTG 2502
Db 2441 GTTGATGAACACTGTAAAGCCATGTTTGAACCCATGATCTGG 2487
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RESULT 7

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US-10-041-018-377
; Sequence 377, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 377
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-041-018-377
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Query Match 26.2%; Score 732.4; DB 7; Length 2506;
Best Local Similarity 59.5%; Pred. No. 2.3e-161;
Matches 1356; Conservative 0; Mismatches 876; Indels 48; Gaps 5;
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QY 270 GGACAACTAATCCCACTAATCTGATCATGATACCAACAAACGATCCAAACACAG 329
Db 143 GTACAGCAAGAGCTAACATGTGAGCTTTGACCAACAAAGAGAGATTAGGAAATG 202
QY 330 TTTAAATAATGTAGAAATTTCTGTTTCTTCATATGACACAGCATGGGTAGCATCCCT 389
Db 203 TTGGAGAAAGTGGAGCTTTCTGTTTCGGCTACGATAGTTGGGTAGCAATGGTTCCA 262
QY 390 TCTCCAACTCACCAAATGCGCTTTTCCCTGAGTGTCTCAATTTGTTAAATTAAT 449
Db 263 TCACCAGCTCCCAAAATGCTCCACTTTTCCCAAGTGTGAAATGGTTATTGGATAAT 322
QY 450 CAGCTTAATGATGTTTCATGGGCTTTGTTAAATCACACTCATATCATATCAATCACTCCCTTG 509
Db 323 CAACATGAAGATGATCTTTGGGACTTGATACCC-----ATGACCATCAATCTCTT 373
QY 510 CTTAAAGATTCTCTATCTTCAACATTAGCATGATTTGTCATTAATAAGATGGAATGTT 569
Db 374 AAGAAGGATGTGTTATCATCTACACTGGCTAGTATCTCGCGTTAAAGAAAGTGGGAAT 433
QY 570 GGGGAAGATCAATAATAAAGGCTTAAGTTTATTGAGTCAATCTTGTCTCAGCTACT 629
Db 434 GGTGAAGACAAATTAACCAAGGCTCTCCAGTTTATTGAGCTGAATTTCTGATAGTCACT 493
QY 630 GAAAAAGTCAACCATCTCCCATTTGTTGACATCATATTTCTGTTTGTCTTGAGTAT 689
Db 494 GATGAAACCATACAGAAACCAAGAGTTGATTTATATTTCTGCGGATTAATAT 553
QY 690 GCGAAAACTTGGACATAAACCTCTCTTCAAAAACAAACAGATTTTAGTTTGTGCTACAT 749
Db 554 GCTAGAGATTTGAATCTGACGATTTCCATTTGGGCTCAGAACTGGTGGATGATCATGATACGA 613
QY 750 AAGAGGAATTTGAGCAAAAAAG-----ATGCCATTTCAATGAGATGGATGATAC 800
Db 614 AAAAGAGATCTGATCTTAAATGTAGTAAAGTTTCAAGGGAAGAGAGCATAT 673
QY 801 TTGCGGTATATCTCTGAAGGACTCGGTAATTTATATGATTGGAATATGGTGAAGAAATAT 860
Db 674 CTGCGCTATGTTTAGAGGGGCAAGAAACCTAAAGATTTGGGATTTGATAGTCAAAATAT 733
QY 861 CAGATGAAAAATGTTCTGTTTTCACCTCAACATCAGCAACAGCTGCTGCTTTTCAATTAAT 920
Db 734 CAAAGGAAAAATGGTCACTGTTTGTATTTCTCCAGCCACACACAGCAGCTGCTTTTACTCAG 793
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Qy	444	AATTAATCAGCTTAAATGATGGTTTCATGGGCTCT-TGTTAAATCACACTCATTAATCAATAATCA	502
Db	280	CAGAATCAGCAGGATGATGGATCTTGGGGTTCAGCCAAATCTGACTCAT-----	328
Qy	503	CCCGTTCGTTAAAGATTCTCTATCTTCAACAAATAGCATGTATTGTCGCATTTAAAAAGATG	562
Db	329	--CGTTCAGCAAGATGTTCTCTATCACTGTCGCAATGTTCTTCGCTTGAAGAGATG	386
Qy	563	GAATGTTGGGGAAGATCAAAATAAAGGTCCTAAGTTTTATTAGATCAAAATCTTGTCTTC	622
Db	387	GAATGTTGGCAGAGAGAACAATTTGGAGAGGACTGCAATTTTCATCGGAGGAATTTCTCTGT	446
Qy	623	AGCTACTGAAAAAAGTCAACCATCTCCGATTTGGTTTTTGACATCATATTTCTGCTTTGCT	682
Db	447	TGCTATGGAACGAGTGTTCACTTCTCTATAGGTTTCAACATCACCTTTCTCGTGTGCT	506
Qy	683	TGAGTATGCGGAAAACTTTGGACATAAAACCTCTTTCAAAAACAAACAGATTTTACTTTTGAT	742
Db	507	TNACCTCGGCATTCGATATGGTTTAGAATTTCTGTAAAGACAAACTGATGCTGTGTGCAT	566
Qy	743	GCTACATAAGAGGGAATTTGGAGCAAAAAAGATGCCA-----TTCAAATGAGATGGA	793
Db	567	TCCTCACCGCGGAGATGGAAATGGAAGGCTGGCTGTGGATAGTTCTTTTGGNAGAAA	626
Qy	794	TGGATCTTTGGCGTATATCTCTGAAGACTCGGTAAATTTATATGATTTGGAAATATGGTGAA	853
Db	627	AGCATATATGGCTTTTATCCAGAAAGATTGCGGAANTATGCTGGACTGGGATCAAGTTAT	686
Qy	854	GAATAATCAGATGAAAAATGGTCTGTGTTTTCAACTCACCATCAGCAACAGCTGCTGCTTT	913
Db	687	GAAGTTTCAGAGGAAGATGGATCAATTTGTCAGCACTCCTTCCACAACCTGCTGTGCAAT	746
Qy	914	CATTAAATCATCAAAATCCTGGTGTCTTAATATTAAATTTCACTTTTGGACAAAGTTTGG	973
Db	747	AATCCACAAATACAAACGACCAAGCCCTTCAATACCTAAATTTGCTTGTCACTGAATTTGG	806
Qy	974	TAATGCAGTCCCAACAGTTTATCCTCATGATTTATTTATCCGACTTTCTATGGTTGACAC	1033
Db	807	CAGTGCAGTACACGAAATGATCCTTCAATGGGTACATGTGCAGCTTTCAATGGTGGACGC	866
Qy	1034	AATTGAAAGATTAGGAAATTTCAACACCATTTCAGAGTGGAAATTTAAAAATGTTTTAGATGA	1093
Db	867	GCTTGAATAAATGGGAATTTCTCAGCGCTTTGTCAAGTGAATAGAAAGCATCTGGACAT	926
Qy	1094	AACATACAGATGTTGGTGGAAACGAGATGAGCAAAATATCATGGAGTTGTFAACATGTGC	1153
Db	927	GGCATACAAATGCTGTGTTACAGAAAGATGAGGAAATCATGATGACATAGCAACATGTGC	986
Qy	1154	TTTTAGCCTTTCCGTTATTAGAGTCAATGGGTATGAAGTTTCCCCAGATCCATTTGGCTGA	1213
Db	987	AATGGCAATTTCCGCTTTTGGAGATGAATGGTTTACAATGTTTCTTCAGATGAGCTGTCTCA	1046
Qy	1214	AATTACTTAATG-----AATTAGCTTTGAAAGACGAATATGC	1249
Db	1047	CGTTGCTGGAGCTTCCACTTTTCCATGATTCACTACAAGGATATTTAAATGATACAAATC	1106
Qy	1250	AGCTCTTGAACATATCATCGGTACATATATTATACCAAGAGATTTATCTTCTCGAAA	1309
Db	1107	CCTACTGGAATTTGTAAGAAGCTTCAAAAGTCACTTATACGAAAAACGATCTGATCTTAGA	1166
Qy	1310	ACAAATCTTGAAGTACGCTGATTTTCTCAAAAGAGATAATCCACTGATTTCAACACAGCT	1369
Db	1167	TGCGATAGGTTCTGGTCTCGCAACTTATTGAAGGATAAGATGCTGTAGTAGGGTGCA	1226
Qy	1370	TTCTTAAATTAATTCACAAAGAGGTGGAAAAATGCTCTTTAAGTTTCCTTATCAATACCGGTTT	1429
Db	1227	AAAAGACTCGATTTTTCGAGAGATGGAGTATGCTGTGTTAAATTTTCCCTTGATTTCCCACT	1286
Qy	1430	AGAACGATTAACACTAGACAAATATACAGCTTTTACAAATGTAGACAAATACAGAAATCT	1489
Db	1287	GGAGCGCTTAGAACACAAGAGAAACATCGAACATTTTGAATGCTTTGGGGTCTCTGATGCT	1346

RESULT 9

RESULT 9
US-10-425-115-22041

US-10-423-113-22041
: Sequence 22041, Application US/10425115

; sequence 22041, Application US/

; PUBLICATION NO: US20
: GENERAL INFORMATION:

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

APPLICANT: LA ROSA, THOMAS J.
APPLICANT: KOVALIC, DAVID K.

;; APPLICANT: KOVALIC, DA
;; APPLICANT: Zhou. Yihua


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Db 1073 CTGCGTGTGATGTCGCAAAAGCATCATGCTCAGCGTGTAGTTGATGACTTCTTCGATG 1132
Qy 1771 TCGGTGTACAAATCGATGATGACCACTGATTCATGTTGTTGAAATGGAATGTAG 1830
Db 1133 TTGGTGGATCAAAAGAGAACAGAAATCTCATCGAAATTAGTTGAGAACTGGGATGAGC 1192
Qy 1831 ATGTCGAAGAAGATTGTTGTTTCAGAGCATGTTTCGATTTTATTTTAGCAATTAAGAATG 1890
Db 1193 ACCACAAAGTTGAGTCTGTTTCGGAGAAAGTAGAAATAGTTTCTATGCTGTCTAATA 1252
Qy 1891 CAATCTGTTGGATTGGAGATGAAGCTTTTAAATGGCAAGCGCGGATGTAACATGAGCATG 1950
Db 1253 CAGTGAACCAAGCTTGGATCTATGCTTCTCAGTACAGAAAGCGGATGTGACAAAACACC 1312
Qy 1951 TTATTCAACTCTGTTGGAACTAATGAATAGTAGTATGTTGAGAGAGCTATATGACAGAG 2010
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Qy 2011 ATGCTTATGTGCCAACATTAATGAATATATATGAAACGCTTACGTGTCTCAATTTGCAATTAG 2070
Db 1373 GGCAATTTGTACCAACAGTTGAGGATACATGSCAAATGCAATGCTTCTCTTGGCACTGG 1432
Qy 2071 GCCCGATTGTCAAGCCGGCTATTATCTTTGTTGGGGCCAAATATATCAGAGGAGATTGTTG 2130
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Qy 2131 AAAGCTCTGAATATCATATCTATTAACTAATATGACGACGCGAGGTCTGCACTTCTAAACG 2190
Db 1493 AAGATCATGAATACAGCAATTTTGTCTGAGTCTATGTTTCACTTGCAGTCGCTCTTAAATG 1552
Qy 2191 ATATCCATAGCTTCAAGAGGGAATTTAAGGAAGCAATTAACGCGGTAGCATTTGCATT 2250
Db 1553 ACATTCGAAGCGTTGAGAGGAGTTTCCAGCTGGTAAATCTGAACAGCGTTTCTACTGCTTG 1612
Qy 2251 TGAGTAAACGAGAAAGTGGGAAAGTGGAAAGAGTGTGGAGGAGATGATGATGATGA 2310
Db 1613 CTCTACACAGTGGTGGTTCATGTCCTAGAGCGGCTAAGAGGAAACACATGGATCTT 1672
Qy 2311 TTAAGAACAGAGAAAGAAATTAATGAATTAATTTTGAAGAAATGGTAGCATTTGTTTC 2370
Db 1673 TAGAGTGTATGAGAGAGGTTTAGTAGCGTTGGTTCGT---AGACAGGACAGTGTGTTTC 1729
Qy 2371 CTAGAGCTCTTAAAGATGCAATTTTGGAAACATGTGTACGTTGTAATTTTTCAGCAA 2430
Db 1730 CTAGTCAATCAAGAGCTGTTCTGGAAGCTTTTGGAGCAATTCACCTGTTCTACTTCC 1789
Qy 2431 ACAGTACGCGGTTTAC 2446
Db 1790 AGATTGATGGATTAC 1805

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RESULT 12

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US-10-425-115-175619
; Sequence 175619, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 175619
; LENGTH: 2364
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_91756C.1

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US-10-425-115-175619
Query Match 15.4%; Score 430; DB 8; Length 2364;
Best Local Similarity 55.7%; Pred. No. 3.4e-90;
Matches 945; Conservative 0; Mismatches 715; Indels 36; Gaps 5;

Qy 778 ATTCAAAATGAGATGGATGATGATCTGCGGTATATCTCTGAAGGACTCGGTAATTTATATG 837
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Qy 838 ATTGGAATATGGTGAAGAAATATCAGATGAATAATGGTTCTGTTTCACTCACTCACTCAG 897
Db 180 ACTGGAATGATGTTATGAAGTTCCAAAGCGAAGATGATCCTTTGTTAACTCTCTCTG 239
Qy 898 CAACAGCTGCTGCTTTCATTAATCATCAAAATCCTGTTGCTTAAATTTAAATTCAC 957
Db 240 CAATCTGCTGCGCTTTTGGTCGCCAATATGACGACAAAGCGCTACAGTATCTAAATTCG 299
Qy 958 TTTTGGACAAGTTTGGTAAATGCAAGTCCCAACAGTTTATCTCATGATTTTATTTATCCGAC 1017
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Qy 1018 TTTCTATGTTGACACAAATTTGAAGATTTAGGAATTTTCAACCAATTTTCAAGATGGAATTA 1077
Db 360 TTTCAATGGTGGACACGCTCGAAAGTGTGGAAATATCAGGCATTTTCTGTGGAGAAA 419
Qy 1078 AAAATGTTTATAGATGAACATACAGATGTTGGGTGGAAAGAGATGAGCAATATTCATGG 1137
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Qy 1138 ATGTTTAAATGATGCTTTTACGCTTTTTCGGTTTATTAAGGATCAATGGGTATGAAGTTTCCC 1197
Db 480 ATGCAGAACATGTCGATGGCAATTTTGAATTTTCAAAATGATGCTTTGATGTTTCCA 539
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Db 540 CAGATTTGTTGTCTCATATTTGCTGAAGCCTCCAAATTTCCATACTCACTACAGGATATT 599
Qy 1234 TGAAGACGAAATATGAGCTCTTTGAAACATATCATGCGTC---ACATATATTTATACCAAG 1290
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Qy 1651 AGACCGCTTACTGTTATTTCTGTTGCTGCAACACTTTTCGTTCCCGAATTTATCAGATG 1710
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Db 1074 CTGCGGTTGATGTCGCAAAAGCATCATGCTCAGCGTTGTAGTTGATGACTTCTTCGATG 1133

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QY 1771 TCGGTGGTACAAATCGATGAATTCACCAACCTGATTCATATGTGTTGAAAAATGGAATGTAG 1830
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QY 1891 CAATCTGTTGGATTTGGAGATGAAGCTTTTAAATGGCAAGCGCGCATGTAACCTAGCCATG 1950
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QY 1951 TTATTCAAACTTGGTTGGAACTAATGAATAGTATGTTTGAGAGAGCTATATGGAAGAAG 2010
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QY 2011 ATGCTTATGTGCCAACATTAATGAATATATATGAAAAACGTTTACGTTGCTATTGCAATTAG 2070
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QY 2071 GCCCGATTTGCAAGCGCGCTATTACTTTGTGGGGCCCAAATTTATCAGAGGAGATTTGTTG 2130
Db 1434 CGGTCATTATCTTCCAGCGCAGTATTTTCTTGGCGAAACGCTCTCAGATTACATGTTCA 1493
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Db 1554 ACATTCGAAGCGTTGAGAGGGAGTTTGAAGCTGTTAACTGAACACGCTTCTACTGCTTG 1613
QY 2251 TGAGTTAACGGAGAAAGTGGGAAAGTGGGAAGAGAGTTTGTGGAGGAGATGATGATGATGA 2310
Db 1614 CTCTACACAGTGGTGTTCATGTCCATAGAACGCGCTAAGAAGGAAACACATGGATCTT 1673
QY 2311 TTAAAAACAGAGGAAAGAAATTAATGAATTAATTTTGAAGAAATTTGTTAGCAATTTGTTTC 2370
Db 1674 TAGAGTCGTATAGGAGAGGTTTAGTAGCGTTGGTTCGT---AGACAGGACAGTGTGTTTC 1730
QY 2371 CTAGAGCTTGAAGATGCAATTTTGAACATGTCACGCTGTTGAAATTTTATTTTACGCAA 2430
Db 1731 CTAGGTCATGCAAGGAGCTGTTCTGGAAGCTTTTGAAGCAATTCACCTGTTCTACTTCC 1790
QY 2431 ACGATGACGGGTTTAC 2446
Db 1791 AGATTGATGAATTTAC 1806
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RESULT 13
US-10-425-114-5988
; Sequence 5988, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5988
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700550363_FLI
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US-10-425-114-5988

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Query Match 14.1%; Score 392.4; DB 7; Length 2029;
Best Local Similarity 53.9%; Pred. No. 2.3e-81;
Matches 999; Conservative 0; Mismatches 741; Indels 112; Gaps 5;

QY 700 TGGACATAAACCTCTTTCCAAAACAAACAGATTTTAGTTTGTATGCTTACATAAGAGGGAAAT 759
Db 4 TGGGTTTAGAATTTCTCTGTGAAGACAAACATGATGTCGTGGCAATCTCTTACCCTGGGAGA 63
QY 760 TGGAGCAAAAAAG-----ATGCCATTCAAAATGAGATGATGATGATGATGATGATGATGAT 810
Db 64 TGGAAATTGAAAGCGCTGGCTGTGGATAGTTCTTTTGGAGAAAAGCATATATATGGCTTTTA 123
QY 811 TCTCTGAAGGACTCGGTAAATTTATATGATGGAATATGTTGGAATATGTTGGAATATATGATGAAA 870
Db 124 TCCAGAGAGGATTCGGAATATATGCTGGAATGCTGGAATCAAGTTATGAAATTTTCAGAGGAAGA 183
QY 871 ATGGTTCTGTTTCAACTCACCACCATCAGCAACAGCTGCTGCTTTTCAATTAATCATCAAAATC 930
Db 184 ATGGATCATTTGTTTACGACTCTCTTCCAAACATGCTGTTGCAATTAATCCAAATACAACG 243
QY 931 CTGGTTGCTTAATTAATTTAAATTTCACTTTTGGCAAAAGTTTGGTATATGAGTCCCAACAG 990
Db 244 ACCAAGCCCTTCAATACCTAAATTTGCTTGTGAGTAAATTTGGCAGTGCAGTACCAGCAA 303
QY 991 TTTATCTCATGATTTATTTATCCGACTTTTATGTTGATGTTGATGATGATGATGATGATGATGAT 1050
Db 304 TGTATCTTCAATGGTACATTTGTCAGCTTTCAATGGTGGACGCTTGGAAAAATGGGA 363
QY 1051 TTTTCACCACTTTCAGAGTGGAAATTTAAATTTTACATGAAACATACAGATGTTGGG 1110
Db 364 TTTCTCAGCGCTTTGTCAGTGAATAGAAAGCATCTCGACATGTCATGATGATGATGATGATGAT 423
QY 1111 TGGAAACGATCAGCAAAATTAATTCATGGATGTTGTAACATGCTGCTTTAGCGCTTTTCGCTTAT 1170
Db 424 TACAGAAAGATGAGGAAATCATGATGGACATAGCAACATGTCATGCAATGGCATTTTCGCTTT 483
QY 1171 TAAGGATCAATGGGTATGAAGTTTCCCGAGATCCATTTGCTGAAATTAATTAATGAATTAG 1230
Db 484 TGAGGATGAATGGTTACAAATGTTTCTCAGATGAGCTGTCTCAGCTTGTGGAGCTTCCA 543
QY 1231 CTTTGAAGACGAATATGCGACTTTGAAA----- 1260
Db 544 CTTTCATGATTCATCAAGGATATTTAAATGATACAAAATCCCTACTCGGAATTTGTACA 603
QY 1261 -----CATATCATGGGTCCACATATATATATACCA 1288
Db 604 AGACCTCAAAAGTCACCTTATCAGAAAACGATCTGATCTTAGATCGCATAGGTTCTCTGTT 663
QY 1289 AGAGGATTTATCTTCTGGAAAAACAAATCTTGAAGTCAGCTGATTTCTCTCAAGAGAGTAAT 1348
Db 664 CTGGCAACTTATTTGAAGGATAAGATGCTGTAGTAGGGTGCAAAAAGACTCGATTTTGG 723
QY 1349 ATCCACTGATTCAAAACAGCGCTTTCTTAAATTAATTTACCA----- 1386
Db 724 GAGAGGTGCTGCAAAAAAAATTTAAATTTCTCAATTTTTCACCTGGAGGTTGATTTATGTC 783
QY 1387 -----AAGAGGTGAAAAATGCTCTTAAGTTCCCTTATCAATACCGGTTTAGAA 1433
Db 784 TGTGTTTTGTGATTTTCAGATGGAGTATGCTGTTAAATTTTCCCTTGTATTTCCACACTGGAG 843
QY 1434 CGCATAAACATCTAGACGAAATATACAGCTTTTACATGTAGACAAATCAAGAATTTCTGAAA 1493
Db 844 CGTCTAGAACACACAGAGAAACATCGAAATTTTGTATGCTTGGGGTTTCTCTGATGCT---A 900
QY 1494 ACTACATATCACTCATCAATATATAGTAACCTGATTACTAGGTTGCTGTTGTAAGAT 1553
Db 901 ACAACAAAATCTCTATCTTTTTCGATCAATCAAGAAATCTTACGCTTTGCGAGTCGAGAT 960
QY 1554 TTTCTACACCTGCGCAATCTATTTTATCGTGAAGAAATTTAAAGGCTTTGAAAGGTGGGTGTA 1613
Db 961 TTCAGTTTCTCTCAAGCTGTTTACCAGGATGAATTTCCGCAATCTTGTATGTTGGGTGAAG 1020
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1614 GAGATAAGTTGGACCAAGCTCAAGTTGTGCTAGGCAAAAGACCGCTACTGTATTTCTCT 1673
1021 GAGACACAGCTGGACCAAGCTACATTTGTCTCGGCAAGAACTGACATATTTCTATCTGTCT 1080
1674 GTTGTGCAACACATTTTGTCTCCGAATATACAGTCGCGGTATTTATCATGGGCAAAAT 1733
1081 GCTGCTGCTACCGTATTTTCTCTGAATTTGTCTGACGCTCGCATTTTCATGGGCAAAAT 1140
1734 GGCATATTAACTACAGTAGTTGATGACTTTTGTGATATCGTGTGTAACATCGATGAATTG 1793
1141 GGTGCTCTCAACTGTGGTGTGATGACTTCTTGATGTTGGTGATCAAAAGAAATTA 1200
1794 ACCAAGCTGATTCATTTGTTGAAAATGCAATGTAGATGTCACAAAGATTTGTGTCA 1853
1201 GAAACCTGTAGCACTAGTTGAGAAATGCGATGCGCACCATGCAGTTGATTTCTATTCG 1260
1854 GAGCATGTTCCGATTTTATTTTAGCAATTAAGATGCAATCTGTTGGATGAGATGAA 1913
1261 GAACAGGTGAAAATAGTATTTTCTGCTATTTATACAAACCACTAGTGAATATGGCTGGAATTG 1380
1914 GCTTTAAATGGCAAGCGCGGATGTAAGTACCATGTTATTCAAACTTGGTTGGAACTA 1973
1321 GCTTCTGACGACCAAGCGCGTATTTACAAACCACTAGTGAATATGGCTGGAATTG 1380
1974 ATCAATAGTATGTTGAGAGAGCTATATGACCAAGAGATGCTTATGTGCCAACATTAAT 2033
1381 TTAAGATCTATGATGTCGAGGAGAGATGCGAGAGATGCCAATATATGACCAAGTTGAA 1440
2034 GAATATATGGAACCGTTACGTTGCTCATTTGCAATTTAGCCCGGATTTGCAAGCGCGCTATT 2093
1441 GAATACATGACAAATGCTGTTGCTCATTTGCACTGGGCGCAATTTGCTGCCAGCATTTG 1500
2094 TACTTTGTGGGCGCAATTTATCAGAGGAGATTTGTTGAAGCTCTGAAATATCATATCTA 2153
1501 TATTTTGTAGGCAAGAGCTATTTAGAGCATGCTGTCAAAGATGAAGAGTACGATAAATTA 1560
2154 TTTAAGCTATATGACGCGAGGCTGCACTTTCTAAACGATATCCATAGCTTCAAGAGGAA 2213
1561 TTTAGGCTAGTACACTTGGGAGGCTCTCTCAATGACTACCAAGTTTAGAGAGGAA 1620
2214 TTTAAGAGGCAAAATTAACCGCGTAGCTATGCTTTGAGTAAACCGAGAGAACTGGGAAA 2273
1621 GGCAACCGAGGGAAGCTGATAGTTGTTCTCTACTTGTGCTCCACAGTGGTGTCTATG 1680
2274 GTGGAAGAGAGGTTGAGGAGAGATGATGATGATTAATTAACCAAGAGGAAAGATTA 2333
1681 TCCATAGAAGCCGTAATAAGGCAATGCAAGATGCCATAGACGTTGCTAGGAGAGACTTG 1740
2334 ATCAAAATTAATTTTGAAGAAAATGGTAGCATTTGTTCTAGAGCTTGTAAAGATGCAATTT 2393
1741 CTAAAGTTGGTTCT---CAGGAAGAAAGTGTGTTCTTAGGCCATGCAAGGAGCTCTTC 1797
2394 TGGAAATGTTGTCACGTTGTTGAATTTTATTTTACGCAACGATGACGCGTTTA 2445
1798 TGGAAATGTTGAAGATCTTCACTTCACTGTTTACTCTCAGAAATGATGATTTA 1849

RESULT 14
US-10-259-194A-107
; Sequence 107, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassemlan, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas

APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/370,620
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 107
LENGTH: 2223
TYPE: DNA
ORGANISM: Oryza sativa
US-10-259-194A-107
Query Match 13.6%; Score 379.4; DB 6; Length 2223;
Best Local Similarity 54.5%; Pred. No. 2.7e-78;
Matches 900; Conservative 0; Mismatches 676; Indels 75; Gaps 4;
795 GGATACCTTGGCGTATATCTCTGAAGGACTCGGTAAATTTATATGATTTGGAATATGGTGAAG 854
574 GAATATACGGCTTATGCTCTCAGAAGGATTAGGCAATATTCAGAACTGGAATGAAGTATG 633
855 AAATATCAGATGAAATATGGTCTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACT 914
634 AAATTCAAAGAAAGAAATGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 693
915 ATTAATCATCAAAATCCTGCTGCTTCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 974
694 GTCCCAACTATGATGCCAAGCTCTCCAGTACTTAGACATGCTCTTGGCAAAATTTTGA 753
975 AATGCACTCCCAACAGCTTTTATCTCATGATTTATTTATCCGACTTTCTATGTTGACACA 1034
754 AGTGCACTGCCAGCGCTTATCTCGCAATATTTTCACTCTCAGCTCTACATGGTGGATGTG 813
1035 ATTGAAGATTTAGGAATTTTCAACCACTTTTCACTCAGATGGAATTTAAATTTTAAATTT 1094
814 CTTGAAAAGATGGAATATCTAGGCATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 873
1095 ACATACAGATGTTGGTGGAAACGAGATGAGCAATATTCATGATGTTGTTGTTGTTGTTGTT 1154
874 ACCTACAGTTGCTGGAACAGAGGATGAGAAATTTGCTTGCATGCAATGCAATGTTGG 933
1155 TTAGCCTTTTCGGTTTAAAGGATCAATGGGTATGAAAGTTTCCCGAGATCCATTTGGCTGAA 1214
934 ATGGCATTTTCTGATGTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993
1215 ATTACTAATGAATTAGCTTTTGAAGAGCAATATGCAAGCTCTTGAACATATATATGCGTCA 1274
994 TTTTCT-----GAACTTTCAAGTTTCCCAATTTCA 1023
1275 CATATATTATCAAGAGGATTTATCTCTGGAAGAAATCTTGAAGTCAAGTCAAGTCAAGTCA 1334
1024 CTTCAAGGATATCTGAATGATCAAGATCTTTATTAGATTAATCAAGGCTTCAAAAGTC 1083
1335 CTCAAGAGATAATATCCACTGATTCACACAGGCTTTCTAAATTAATTTCAAAAGAGGTG 1394
1084 -----AGTATCGCAAGAAAGGAGTTT 1104
1395 GAAATGCTTTAAGTTCCCTATCAATACCGGTTTAGAAGCAATCACTAGACGAAAT 1454
1105 GAATATGCTCTTGAATTTCCCTTCTATACCATCTTGGATCGTCTAGACCAATAAAGAAAT 1164
1455 ATACAGCTTTACATGTTAGCAATACAGAAATTTCTGAAACTACATATCATCTCAAT 1514
1165 ATCGAAATTTTGAATTAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1221
1515 ATTAGTAACACTGATTTACCTAAGGTTGGCTGTTGAAAGATTTTCTACACCTGCGCAATCTATT 1574

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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 77869
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17103C.1
; US-10-425-115-77869

Query Match      12.8%; Score 357.4; DB 8; Length 2178;
Best Local Similarity 54.8%; Pred. No. 4,1e-73;
Matches 793; Conservative 0; Mismatches 621; Indels 33; Gaps 3;

QY 1026 GTTGACACAAATTGAAGATTAGGAATTTACACACCATTTCAGAGTGGAAATTTAAAATGTT 1085
DB 464 GTGATGTGCTTTGAAACAATGGGATTTCTCGCATTTTGGTGGTGAATCAAGTGTATC 523
QY 1086 TTAGATGAACAATACAGATGTTGGGTGGAACGAGATGAGCAATATTTCAATGATGTTGTA 1145
DB 524 CTGTGACAGACATACAGATGTTGGTTACAGACACGAGGAATTTATGACGACACAACG 583
QY 1146 ACATGTCTTTAGCTTTTCGGTTATTAAGGATCAATGGGTATGAAGTTTCCCGAGATCCA 1205
DB 584 ACATGTGCGATGGCATTTTCGTATTTCAAGGATGAATGGATACAATGCTCTCTCTGATGAG 643
QY 1206 TTGGCTGAAATTTACTAA-----TGAATTAGCTTTTGAAGAC 1241
DB 644 TTGTATCATGTTTGTGAAGCTTCGAGCTCCATAATTCATCTGGAGGATATCTCAATGAC 703
QY 1242 GAATATGACGCTCTTGAACAATATCATGCGT---CACATATATATACCAAGAGGATTTA 1298
DB 704 ACAGAACTCTTTAGAAATTAACAAGGCTCTACAGTTAGTATCTCTGAAGACGAGTCT 763
QY 1299 TCTTCTGGAACAAATCTTTGAAGTCAGCTGATTTCTCAAGAGATATATATCCACTGAT 1358
DB 764 ATCTCTGGATAGCATAGGCTCAAGGTCAAGTACTTACTGAGGGAACAACCTAGAGTCTGT 823
QY 1359 TCAACAGCGCTTCTAAATTAATTCACAAGAGGTGGAAATGCTTAAAGTTCCCTATC 1418
DB 824 GGTGCTCTACGAAATCTCTTCACTCTTTAAAGAGGTGGAAACATGCTCTGACGCTCCCTTC 883
QY 1419 AATACCGGTTTGAACGCAATAACACTAGACGAAATATATACAGCTTTTCAATGTAGACAAT 1478
DB 884 TACACCAATTTGACCGCTACACCATAGGTGGAACATCGAAATTTCAATATATAGAG 943
QY 1479 ACAAGAAATTCGAAACACTACATATCACTCATCAAAATATTTAGTAACTACTTACCTAAGG 1538
DB 944 CAGCACATCTAGAGACACCATATCTGTCAAATCAACATACCAGTAGAGATATCTTAGCG 1003
QY 1539 TTGGCTGTTGAAGATTTCTACACCTGCCAATCTATTTATTCGTGAAGAAATTTAAAGTCTT 1598
DB 1004 TTGAGTATTTAGAGACTTCTAGTTTCTCTCAGTTTACTTCTCAGCAAGAACTTCAACATCT 1063
QY 1599 GAAAGTGGTGGTAGAATAAAGTTGGACACGAGCTCAAGTTTGTAGGCAAAAGACCGCC 1658
DB 1064 GAAAGCTGGTGAAGAGTGACAGTTAGACAGCTACAAATTTGCGCGACAGAAAGTTGGCA 1123
QY 1659 TACTGTTATTTCTGTGTGCTGCAACACTTTTCGTCTCCGAAATATTCAGATGGCGGTAT 1718
DB 1124 TACTTCTACTTGTCTGCTGCGCACCATGTTCTCTCTCTGAGCTGTCTGATGCTCGAACT 1183
QY 1719 TCATGGGCAAAATGGGCATATTAATCAAGTAGTTGATGACTTTTTCATATCGGTGT 1778
DB 1184 TTGTGGGCAAAATTTGGTGTGCTCAACATATTTGTTGACGACTTCTTTGATGTTGCGGGA 1243
QY 1779 ACAATCGATGAATTCACCAACCTGATTCATGTTGTTGAAATTTGGAATGTAGATGTCGAC 1838
DB 1244 TCAAAAGAGAACTTCGAAACCTTGTCTGTTGGTTGAGATGTGGGACGAGCATCAAAA 1303
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RESULT 15

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US-10-425-115-77869
; Sequence 77869, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 05:56:03 ; Search time 483.49 Seconds
(without alignments)
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	782.2	28.0	2658	3	US-08-727-308-2
2	782.2	28.0	2658	3	US-08-727-308-3
3	453.2	16.2	2403	3	US-09-614-912-23
4	238.2	8.5	1157	3	US-09-614-912-33
5	194.8	7.0	2861	3	US-09-398-395A-55
6	194.8	7.0	2861	3	US-09-887-586A-55
7	194.8	7.0	2861	3	US-09-895-752-55
8	194.8	7.0	2861	3	US-09-903-012B-55
9	194.8	7.0	2861	3	US-09-900-797-55
10	194.8	7.0	2861	3	US-09-893-820-55
11	194.8	7.0	2861	3	US-10-041-007-3
12	153.8	5.5	2700	3	US-09-315-861-1
13	153.8	5.5	2700	3	US-09-398-395A-43
14	153.8	5.5	2700	3	US-09-887-586A-43
15	153.8	5.5	2700	3	US-09-895-752-43
16	153.8	5.5	2700	3	US-09-903-012B-43
17	153.8	5.5	2700	3	US-09-593-253-1
18	153.8	5.5	2700	3	US-09-900-797-43
19	153.8	5.5	2700	3	US-09-893-820-43
20	139.2	5.0	531	3	US-09-614-912-27
21	133.8	4.8	2241	3	US-10-041-007-38
22	133.8	4.8	2388	3	US-10-041-007-36
23	133.8	4.8	2445	3	US-10-041-007-34
24	133.8	4.8	2622	3	US-10-041-007-32

Sequence 1, Appli
Sequence 25, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 1, Appli
Sequence 15, Appl
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Sequence 45, Appl
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Sequence 45, Appl
Sequence 45, Appl
Sequence 14, Appl
Sequence 39, Appl
Sequence 37, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 12, Appl

25 133.8 4.8 2705 3 US-10-041-007-1
26 130.6 4.7 468 3 US-09-614-912-25
27 120.8 4.3 2528 3 US-09-234-393-41
28 120.8 4.3 2528 3 US-09-865-171-41
29 119.2 4.3 2424 3 US-09-234-393-1
30 119.2 4.3 2424 3 US-09-360-545-15
31 119.2 4.3 2424 3 US-09-865-171-1
32 119.2 4.3 2424 3 US-09-398-395A-45
33 119.2 4.3 2424 3 US-09-887-586A-45
34 119.2 4.3 2424 3 US-09-895-752-45
35 119.2 4.3 2424 3 US-09-903-012B-45
36 119.2 4.3 2424 3 US-09-900-797-45
37 119.2 4.3 2424 3 US-09-893-820-45
38 119.2 4.3 2424 3 US-10-041-007-14
39 119.2 4.3 2525 3 US-09-234-393-39
40 119.2 4.3 2525 3 US-09-865-171-39
41 119.2 4.3 2528 3 US-09-234-393-37
42 119.2 4.3 2528 3 US-09-865-171-37
43 119.2 4.3 2528 3 US-10-041-007-13
44 119.2 4.3 2571 3 US-09-234-393-12
45 119.2 4.3 2571 3 US-09-865-171-12

ALIGNMENTS

RESULT 1
US-08-727-308-2
; Sequence 2, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-727-308-2

Query Match 28.0%; Score 782.2; DB 3; Length 2658;
Best Local Similarity 61.3%; Pred. No. 2.3e-191;
Matches 1390; Conservative 0; Mismatches 823; Indels 54; Gaps 6;

Qy	275	AAC	TAATCCCACTAATCTGATCATTTGATACAAACAAAGAACGGATCCAAAAACAGTTTAA	334
Db	236	AAC	TAAACATGGAGCTTTGCACTTTGAAGAAACAAAGAAAGAAATTAAGAAATTTGTCGA	295
Qy	335	AAAT	GTAGAAATTTCTGTTCTTCATATGACACAGCATGGGTAGCTGGTCCCTTCTCC	394
Db	296	CAAG	GTGAACCTTTTCAGTTCTGCAATATGATACTGCAATGGGTGGCAATGGTTCTCTCTCC	355
Qy	395	AAAC	CTCACCAAAATCGCCTTGTTCCTCTGAGTGTCTCAAATGGGTAAATTAATAATCAGCT	454
Db	356	AAAC	CTCTCAACCAACCTCTTTTCCCGAGTGTATAAATCTGGGTATTAGTAGTCAACA	415
Qy	455	TAAT	GTAGTGGTTTCATGGGGTCTTTGTTAATACACACTCATATAATCAATCAATCACCCGTTGCTTAA	514
Db	416	TGCT	GTATGGCTCATGGGGCTTACTCCCAAC-----GATCAGATTGCTGATGA	463
Qy	515	AGATT	CTCTATCTTCAACATTTAGCATGTATTGTTGCAATTAAGAGATGGAATGTTGGGA	574
Db	464	GGCC	AACTCTTATCTACATAGCATGTGTTCTTACTCTTAAGCGGTGGAAATATGGGCA	523
Qy	575	AGAT	CAAAATAAATAAAGGTCTAAGTTTATATAGTCAAAATCTTGCTTCAGCTACTGAAAA	634
Db	524	TGAT	CATATGAGCAAGGCCCTTGATTTTTATCAAGTCTAATATAGCTTCAGCTACTGATGA	583
Qy	635	AAGT	CAACCATCTCCCAATGGTTTGTGACATCATATTTCTCTGTTTCTTCAGTATGGCA	694
Db	584	GAAC	CAACGTTTCTCCGGTGGGATTTGCAATTTATTTCCCTGGCATGATTCAGTATGCTAA	643
Qy	695	AAACT	TGGACATAAACTCTCTTCCAAACAAACAGATTTTATGTTGATGCTACATAAGAG	754
Db	644	AGACT	TGAAATTTGAAATCTACCTTGGCACCGACGAACTGGATGCCCTTGGTTCGAAGAA	703
Qy	755	GGAA	TTGGAGCAAAA-----AGATGCCATTCAAATGAGATGAGTGGATCTTGGCGTA	808
Db	704	AGAG	TGGAGCTGAGAAAGCTGCAAGACCACTCTGAAGGTGGAAAAACCTTATTTAGCGTA	763
Qy	809	TATCT	TGAAGGACTCGGTAAATTTATATGATTGAATATCGTGAAGAAATATCAGATGAA	868
Db	764	TGTT	TCAGAAGGAATTCGAAAGTTTACAGGACTCGGGATATGGTCATGCAATATCAAAGGA	823
Qy	869	AAAT	TGGTTCTGTTTCAACTCACCATCAGCAACAGCTGCTGCTTTCAATTAATCATCAAAA	928
Db	824	GAAT	TGGATCACTGTTTAATCTCCATCCACTACGCGAGCGCTTTTATGCATAGAATGA	883
Qy	929	TCCT	TGGTTGCTTAATTTAAATTCATCTTTTGGACAAGTTTGGTAAATGCAGTCCCAAC	988
Db	884	TGAT	TGGCTGTTTTCGATTATCTTCGCTCACTCTTACAAAAGTTTGTAGTGGCTCAGTTCCAC	943
Qy	989	AGTT	TATCCCATCATTTATTTATCCGACITTTCTATGTTGCACACATTCGAAGATTAGG	1048
Db	944	AATAT	ATCCTCTTGATATATATGCTCGAATACACATGGTGTATAGCCCTTCAAAAATTCGG	1003
Qy	1049	AAAT	TTCAACCATTTTCAGAGTGGAAATTAATAATGTTTATAGTGAACATACAGATGTTG	1108
Db	1004	AAAT	TGCTCGGCAATTCAAAGAGGAGATTAGAGCGTATTAGATGAACATTTACAGGTGTTG	1063
Qy	1109	GGT	GGAAACGAGATGAGCAAAATATTTCATGAGATGTTGTAAATGCTCTTTAGCCTTCGGTT	1168
Db	1064	GAT	GCAAGGAGAGAAAAATATTTCTTAGATGCTTCAACTTTGTGCAATGCGCTTTTCAAT	1123
Qy	1169	ATT	TAAGGATCAATGGGTATGAAGTTTCCCGAGATCCCAATCGCTGAAATTAATA-----	1222
Db	1124	GTT	ACGTGTTGAAGGATATGATGTTTCTTCAGACCAGTTGACTCAATTTTCAGAGATAT	1183
Qy	1223	-----	TGAAATTAGCTTTGAAAGAGCAATATGCACTCTTGCAAGTCTTTGAAACATATCA	1267
Db	1184	CTTT	CCCCAAATTCGCTTCGGAGATTTTAAAGAGCTTCGGTGCCTCGCTGGAGTTATATA	1243
Qy	1268	TGCG	TCACATATATATACCAAGAGGATTTATCTTCT---GGAAAAACAATCTTGAAGTC	1324
Db	1244	GGCT	CTCAGATATACGCAACCCCGATGAATCTGTTCTGGAATAATAAATCTTTGAC	1303

Qy	1325	AGCTGATTTCTCCTCAAAAGAGATAATATATCCACTGATTCAAAACGCGTTTCTTAAA-----	1376
Db	1304	TAGTCGTTTCTCCTGAAGCATGGATATATCTAGTGAATTCAGTTTGGTCTGTATAGAAACCGATAG	1363
Qy	1377	-TTAAATTCACAAAGAGGTGGAAAATGCTCTTAAGTTTCCCTATCAATACCAATCCGGTTTGAACAG	1435
Db	1364	TGTTGTTTAAACAAGAGCGCTGTAAATGCTCTTGAGTTTCCCTATTAATGCAACTCTAGAACG	1423
Qy	1436	CATAAAACACTAGACGAAATATACAGCTTTTACAATGTAGACAAATACAGAATTTCTGAAAAAC	1495
Db	1424	CCTAAATAAGTTAAGAGGGCAATGGAAGTTTACAGTGGAGACATTTGTGAGGATTTTCAAAATC	1483
Qy	1496	TACATATCACTCAATCAAAATATTAAGTAACACTGATTAACCTAAAGTTGGCTGTGTTGAAGATT	1555
Db	1484	GCCATATGCCCTGTCTTAAATTTTGGCCCATCAAGATTTTCTGGAACCTTGTCTGTAGAGGATTT	1543
Qy	1556	CTACACTGCGCAATCTATTTATCGTCGAAGAAATTAAGAAGTCTTGAAGGTGGGTGGTGTAGA	1615
Db	1544	CAATACCTCGCAACGCATTCATCTTAAAGAACTGGAAGAGCTTCAAAGATGGGTGGTTGA	1603
Qy	1616	GAATAAGTTGGACCAGCTCAAGTTTCTGTAGGCAAAAGACCGCTACTGTATTTCCTCTGT	1675
Db	1604	AAACAAATTTGACGAGTTTGAATTTTTTCAGCTGCACCTAGGCTACTGTCTATTTTCTCTGC	1663
Qy	1676	TGCTGCAACACTTTTGTCTCCCGAATATCAGATGCGCGTATTTTCAATGGCGCAAAATGG	1735
Db	1664	GGCAGCGACCTTTACTGATCCTGAACTTCATGATGCTCGCATAGCATGGGCACAAAATGG	1723
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Db	1724	TGTGCTCACACCCTGGTGTGATGATTTCTATGATGTTGGAGGATCTGAAAGAGNAITGGA	1783
Qy	1796	CAACCTGATTTCAATGTGTTGAAAAATGGAATGTAGATGTGCGACAAAGGATTTGTTTTCAGA	1855
Db	1784	TAACCTTATAGAAATTTGGTGGAAAAGTGGGATCCTGATGGGAAGTGGTTACTGTTCCTAA	1843
Qy	1856	GCATGTTTCGGATTTTATTTTTAGCATTAAGAAGTGCATCTGTGTGATTTGGAGATGAAGC	1915
Db	1844	GGAGCTTTGAGATTTGTTATTTCTTGCACTGCACACAGCATTTTGTGAAATAGGAAGAAGAGC	1903
Qy	1916	TTTTTAATGCGAAGCGCGATGTAACCTAGCCATGTTATTTCAAACTTGGTTCGAACCTAAT	1975
Db	1904	TTTAGTATGCGAAGGACGCACTGTTATAGGAATGTTATCGATGTTGGTGGTCTGCT	1963
Qy	1976	GAATAGTATGTTGAGAGAAGCTATATAGGACAAGAGATGCTTATGTGCCCAACTTAATAGA	2035
Db	1964	GAAGTGATGAGAAAGGAAGCTGAATGGTTCGCAAAATAGGTAGTGTCCATCAATGGGTGA	2023
Qy	2036	ATATATGGAACCGCTTACGTGTCAATTTGCAATPAGGCCCGATTTGTCAAGCGCGCTATTTA	2095
Db	2024	ATATATGGAACAAGCCCATGTATCAATTCGCGTTGGGACCTATAAATCCTTCCAATGCTCTT	2083
Qy	2096	CTTTTGGGGCCCAATTTATCAGAGGAGATTTGTTGAAAGCTCTGATATATCATATCTAAT	2155
Db	2084	CTTTGTTGGACCTTAAACTCTCAGAGGAATGATTTGGAAGCTGTGAATACAGAAAGTTATA	2143
Qy	2156	TAAGCTTAATCAGCACGCGGTCGACTTCTTAAACGATATCCATAGCTTCAAAGAGGGAAAT	2215
Db	2144	TAAGCTGATGAGCACTGCTGCTGCTTGAAGATGATATTCGATCTTACGATAGAAATG	2203
Qy	2216	TAAGGAAGGCAATTAACCGCGGTAGCATTTGCAATTTTGTAGTAAAGGAGAAAGTGGGAAAGT	2275
Db	2204	CAAAGAGGGAAGCTGAATATTCTGTCTCTGTGGATGATTTGATGGCGGTGGTAAATGTCAC	2263
Qy	2276	GGAAGAGAGAGCTTTGTGGAGGAGATGATGATGATTAATAAACAAGAGGAAAGAAATTAAT	2335
Db	2264	CAAAGAGGAGGCCATTTGAAGCAATTAAGAGGGGATTTTGTAGAGGGCGCATTAAGAGCTGCT	2323
Qy	2336	GAATTTAAATTTTGAAGAAATGGTAGCATTTGTTCTCTAGAGCTTTGTAAAGATGCATTTTG	2395
Db	2324	GGGGTTAGTTTTCGACGAGAGAACACTACAA---TTCCAAGAGCTTTGAGGATTTGTTGTTCTG	2380
Qy	2396	GAACATGTGTACAGCTGTGTAATTTTTTTTTTTCGCAAAACGATGACGGGTTTACTGGAAACAC	2455

Db	1544	CAATACCTCGCAACGCATTCATCTCTAAAGAACTCGAAGAGCTTCAAAGATGGGGTGGTTGA	1603
Qy	1616	GAATAAGTTGGACACAGCTCAAGTTTGTCTAGGCAAAAGACCGCTACTGTATTCTCTCTGT	1675
Db	1604	AAACAAATTGGACGAGTTGAAATTTTTCAGACTGCACCTAGGGTACTGCTATTTTGCTGC	1663
Qy	1676	TGCTGCAACACTTTCGTCTCCGAATATTACAGATGCCGGTATTTCATGTCGGGCCAAAATGG	1735
Db	1664	GGCAGCACCCCTTACTGATCTCGAATTCATGATGCTCGCATAGCATGGGCACAAAATGG	1723
Qy	1736	CATATTAACTACAGTAGTTGATGACTTTTTTTTGATATCGGTGGTACAATCGATGAATTTGAC	1795
Db	1724	TGTCTCAGACCGGTGGTTGATGATTTCTATGATGGTGGAGATCTGAAGAGGAATTTGGA	1783
Qy	1796	CAACCTGATTCAATGTGTGAAAATGGAATGTAGATGTCGCAAGGATTTGTTTTCAGA	1855
Db	1784	TAACCTTATAGAATTTGTTGGNAAGTCGGATCCTGATGGGGAAGTGGTTACTGTTCCAA	1843
Qy	1856	GCATGTTCCGATTTTTATTTTTAGCAATTAAAGATGCAATCTGTGTTGGATTTGGAGATGAAGC	1915
Db	1844	GGACGTTTGAGATTGTATTTCTTGCACTGCACAGCACAGATTTGTGAAATAGGAAGAAGGC	1903
Qy	1916	TTTTTAATGCGNACCGCGCATGTACTAGCCATGTTATTCMAACTTGGTTTGGNACTAAT	1975
Db	1904	TTTAGTATGGCAAGGACGCACTGTTATGAGAAATGTTTATCGATGGTTGGTTGGCTCTGCT	1963
Qy	1976	GAATAGTATGTTGAGAGAAGCTATATGGAACAAGAGATGCTTATGTGCAACATTTAAATGA	2035
Db	1964	GAAGTGATGNAAGAAAGNAGCTGNAATGGTGCACAAATTAAGTAGTGCCTCAATGGGTGA	2023
Qy	2036	ATATATGGAAAAACGTTTACGTTGTCATTTGCAATTAGGCCGATTTGTCAAGCCGCTATTTA	2095
Db	2024	ATATATGGAAACNAGCCCATGTATCAITTCGGGTTGGGACCTATAATCCTTCCAATGCTCTT	2083
Qy	2096	CTTTTGTGGGGCCAAAATTATCAGAGGAGATTTGTGAAGCTCTGAAATATCATATCTATT	2155
Db	2084	CTTTTGTGGAACCTAAACTCTCAGAGGAAATGATTTGGAAGCTGTGAAATACCAGAAGTTATA	2143
Qy	2156	TAAGCTAATGAGACGCGAGGTCCAGCTTCTAAACGATATCCATAGCTTCAAGAGGGAATT	2215
Db	2144	TAAGCTGATGAGCACTGCTGTTGCTGCCCTTAAGNATGATATTTCGATCTTACGATAGAGATG	2203
Qy	2216	TAAGGAAGGCAAAATTAAACCGGTPAGCATTTGCATTTGAGTAACGGAGAAAGTGGGAAAGT	2275
Db	2204	CAAAAGGGAAAAGCTGAATTTCTGCTCTGTGGATGATTTGATGGCGGTGGTAATGTCCAC	2263
Qy	2276	GGAAGAAGAGGTTGTGAGGAGATGATGATGATTAATAAAACNAGAGGAAAGNATTAAT	2335
Db	2264	CAAAAGGAGGCCCAATTGAAGCAATTAAGGGGATTTTGTGAGGGCGCATATAGAGAGCTGCT	2323
Qy	2336	GAATAATTAATTTTCAAGAAAATGTTAGCATTTGTTCTCTAGAGCTTGTAAAGATGCATTTTG	2395
Db	2324	GGGGTTAGTTTTCAGGAGAACACTCAAA---TTCCAAGAGCTTGTGAAGGATTTGTTCTG	2380
Qy	2396	GAACATGTGTCAGCTGTTTGAATTTTTTTTTTACGCAACGATGACGGGTTTACTCGAAAACAC	2455
Db	2381	GAATTCATGTCCATTTGTAATCTATTTTACATGGAAGATGATGGGTACACTTCCAATAG	2440
Qy	2456	GATTCCTTGATCTGTGAAGGACATCATTTTACAACCCGTTGGTGTCTG	2502
Db	2441	GTTGATGAACACTGTAAAGAGCATGTTTGTGAACCAACCCATGGATCTGG	2487

RESULT 3

US-09-614-912-23

; Sequence 23, Application US/09614912

; Patent No. 6677502

: GENERAL INFORMATION:

: APPLICANT: Allen. Steve

APPLICANT: Rafalski, Antoni

REEDICANT: KALABRA, MICHAEL
: APPLICANT: Orozco, Buddy

APPLICANT: Miao Gou-Hai

APPLICANT: FAMODU OMOJAYO O.
AFFILIATE: MIAB, GOU-HAU

Db 612 ATGGGAATTTCTCAGCGTTGTGTCAGTGAATAGAAAGCATCCTGGACATGGCATACAAT 671
Qy 1104 TGTGGGTGGAAACGAGATGAGCAATATTCATGATGTTGTACATGTCGCTTTAGCCCTTT 1163
Db 672 TGCTGGTTACAGAAATGATGAGAACTCATGATGACATAGCAACATTTGCAATGGCAATTT 731
Qy 1164 CGGTTATTAAGGATCAATGGGTATGAAGTTTCCCGAGATCCATGGCTGAAATTTACTAAT 1223
Db 732 CGCCTTTTGAGGATGATGGTTAGCATGTTTCTCAGATGAGCTGCTCAGTTGCTGGA 791
Qy 1224 G-----AATTAGCTTTGAAAGCAAGATATGACGCTCTTTGAA 1259
Db 792 GCTTCCACTTTCCATGATTCACACAAGGATATTTAAATGATACAAATCCCTACTGAA 851
Qy 1260 ACATATCATGGTCACA---TATATTATACAGAGATTTATCTTCTGGAACAACATC 1316
Db 852 TTGTACAAGACCTCAAAAGTCACCTTATCAGAAACGATCTGATCTTTAGATGCGCATAGGT 911
Qy 1317 TTGAAGTCAGCTGATTTCTCAAGAGATAATATCCAC----- 1354
Db 912 TCCTGGTCTGGCACTTATGAAGATAAGATGCTGTAGTAGGTGCAAAAGACTCGA 971
Qy 1355 -----TGATTCAAACAGGCTTTCTAAATTAATTCACA----- 1386
Db 972 TTTTGGAGAGATGCTGCAAAACAAAATTTAAATTTCTCATTTTCACTTGGAGGTTCAAGTT 1031
Qy 1387 -----AAGAGGTGAAATGCTCTTAAGTTCCTATCAATACCGGT 1427
Db 1032 TATGTCGTGTTTGTGNTTTCAGATCGAGTATGCTGTAAATTTTCCCTTGTATTCACA 1091
Qy 1428 TTGAAGCGCTAAACACTAGACGAAATATACAGCTTTTACAATGTAGACAATACAAAGATT 1487
Db 1092 CTGGAGGCTTAGACACAGAGAAACATCGAACATTTTGAATGCTGGGGTCTCTGATG 1151
Qy 1488 CTGAAACTACATATCTCATCAATATTAAGTAACACTGATTAACCTTAAGGTTGGCTGTT 1547
Db 1152 CT---AACAACAAAATCCTCATCTTTTCGTATCAATCAAGAAATTCCTAGCTTTGGCAGTC 1208
Qy 1548 GAAGATTTCTACACCTGCCAATCTATTTATCGTGAAGAAATTAAGAGTCTTGAAGGTGG 1607
Db 1209 GAAGATTTCAAGTTTCTCTCAACGTTTACCGGATGAACCTTCGGCATCTTGTAGTTGG 1268
Qy 1608 GTGTAGAGATAAGTTGGACCACTCAAGTTTCTAGGCAAAAGACCGCTACTGTTAT 1667
Db 1269 GTGAGAGAACAGCTGGACCACTCAATTTGCTCGGACGAACTGACATATGCTAT 1328
Qy 1668 TTCTCTGTTGCTGCAACACTTTCTGCTCCGAATTTATCAGATGCGGTATTTTCATGGGCC 1727
Db 1329 CTGCTGCTGCTGCTACCGTATTTTCTCTGAAATGCTGAGCGCTGCAATTTTCATGGGCC 1388
Qy 1728 AAAAAAGGATATTAACACAGATGTTGATGACTTTTTCATATCGTGTGATCAATCGAT 1787
Db 1389 AAAAAAGGTCCTCACAACCTGTTGATGACTTTCTTCGATGTTGTTGGATCAAAAGAA 1448
Qy 1788 GAATTGACCACTGATTCAATGTTGAAATGGAATGTAGATGTCGACAGGATGTTGT 1847
Db 1449 GAATTGAAACCTGATAGCACTAGTTGAGAAATGCGATGGCCACCATGCAAGTTGAGTTC 1508
Qy 1848 TGTTCAGAGCATGTTTCGGATTTTATTTTATAGCATTAAGATGCAATCTGTTGATTTGGA 1907
Db 1509 TATTCGGAACAGGTGAAATAGTATTTTCTGCTATTTATACACAGTGAACCATCTTGA 1568
Qy 1908 GATGAGCTTTTAAATGGCAAGCGCGGATGTAAGTATAGCCATGTTTATCAACTGGTTG 1967
Db 1569 GCAATGGCTTTCTGAGCACAAGCGCGGTGCTTACAAACCACTAGTAGAATATGCTG 1628
Qy 1968 GAACTAATGATAGTATGTTGAGAGAGCTATATGGACAGAGATGCTTATGTCGCAACA 2027
Db 1629 GATTTGTTAGATCTATGATGGTGGAGGCAAGATGGCAGAGATGCCAATATGTACCAACA 1688
Qy 2028 TTAATGAATATATGGAACCGCTTACGTGCTCATTTTGCATTAGGCCCGATTTGTCAAGCCG 2087

Db 1689 GTTGAAGATATACATGACAAATGCTGTTGTCTCAATTTGCACTGGGCCCAATTTGCTGCCA 1748
Qy 2088 GCTATTTTACTTTCTGGGGCCCAATATATCAGAGAGATTTGTTGAAAGCTCTGAATATCAT 2147
Db 1749 GCATTTGATTTTGTAGGGCAAGAGCTATTAGAGCATCTGTCAAAGATGAAGATGACAT 1808
Qy 2148 AATCTATTTAAGCTTAATGAGCAGCGAGGTCGACTTCTTAACGATATCCATAGCTTCAAG 2207
Db 1809 AAATTTATTAGCTAGTAGCAGCTTTCGGGGAGGCTCTCAATGACTACCAAGTTTAGAG 1868
Qy 2208 AGGAATTTAAGAGGCAAAATTAACGCGGTAGCATTTGATTTAGTAACGAGGAAAGT 2267
Db 1869 AGGAAGGCAACGAGGGAAGCTCAATAGTGTCTCTACTTGTGCTCCACAGTGGTGT 1928
Qy 2268 GGGAAAGTGAAGAGAGGTTGTGGAGGAGATGATGATGATTAATAAACAAGGAAA 2327
Db 1929 TCTATGTCATAGAGCCGCTAAAAGGCAATGAGAAAGTCCATAGACGTTCTTAGGAGA 1988
Qy 2328 GAATTAATGAATTAATTTTGAAGAAAATGCTAGCATTTGTTCTAGAGCTTTGTAAGAT 2387
Db 1989 GACTTGTCTAAGTTGGTTCT---CAGGAAGAAAGTCTGTTCTTAGGCCATGCAAGGAG 2045
Qy 2388 GCATTTTGAACATGTCACGTTGGAATTTTTTTTACGAAACGATGACGGGTTTA 2445
Db 2046 CTCTTCTGGAAGATGTGTAAGATACCTTCACCTGTTTACTCTCAGAAATGATGGATTTA 2103

RESULT 4

US-09-614-912-33
; Sequence 33, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
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; LOCATION: (1136).. (1137)
; NAME/KEY: unsure
; LOCATION: (1155)
US-09-614-912-33
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Query Match      8.5%; Score 238.2; DB 3; Length 1157;
Best Local Similarity 58.1%; Pred. No. 38-51;
Matches 433; Conservative 0; Mismatches 303; Indels 9; Gaps 1;

QY 505 CGTTGCTTAAAGATTCTCTATCTTCAACATTAGCATGTATTGTCATTAAAAAGATGGA 564
Db 54 CGGTCAACAANGATGTTCTCCTATCCAGTTGGCATGTGTTCTTGCGTTGAAGAGATGGA 113
QY 565 ATGTTGGGGAAGATCAAAATAAAAGTCTAAAGTCTAAGTTTATTGAGTCAAAATCTTGCTTCAG 624
Db 114 ATGTTGGCAGAGAGAAACAATTTGGAGAGGACTGCATTTTCATCGGAGGAATTTCTCTGTTG 173
QY 625 CTACTGAAAAAAGTCAACCATCTCCCATGTTGGTATGACATCATATTTCTGTTGCTTGGCTTG 684
Db 174 CTATGGACGAGCAGTTCACTTCTCTATAGGTTTCAACTTCCACCTTCTGTTGCTTCA 233
QY 685 AGTATGCGAAAAAATTTGGACATAAACCTCTCTTTCAAAACAAACAGATTTTAGTTGATGC 744
Db 234 GCCTGGCATTTGATATGGTTTAGAATTTCTGTGAACAAATGATGTTCTGTGGCATTC 293
QY 745 TACATAAGAGGGAATTTGGAGCAAAAAAG-----ATGCCATTCAAAATGAGATGGATG 795
Db 294 TTCACCGCGGAGATGGAATTTGAAAAGGCTGGCTGTGGATAGTTCTTTTGGAGAAAAG 353
QY 796 GATACTTGGCGTATATCTCTGAAGACTCGGTAATTTATATATGATGGAATATGGTGAAGA 855
Db 354 CATATATGGCTTTTATCCAGAAAGATTCGGAATATGCTGGACTGGGATCAAGTTATGA 413
QY 856 AATATCAGATGAAAAATGTTCTGTTTCAACTCACCATCAGCAACAGCTGCTGCTTCA 915
Db 414 AGTTTCAGAGGAAGATGGATCATTTGTCAGCACTCTTCCACAACCTGCTGTGCAATTAA 473
QY 916 TTAATCATCAAAATCCTGGTTGTTCTTAATTTATTTAAATTCACCTTTTGGACAAGTTTGGTA 975
Db 474 TCCACAAATACAAACGACCAAGCCCTTCAATACCTAAATTTGCTTGTCAATGAATTTGGCA 533
QY 976 ATGCAGTCCCAACAGTTTATCTCTCATGATTTATTTATCCGACTTTCATATGTTGACACAA 1035
Db 534 GTGCAGTACCAAGCAATGTATCCTTCAAGGGTACATTTGTGAGCTTTCAATGGTGGACGCGC 593
QY 1036 TTGAAAGATTAGGAAATTTTCCACACCATTTTCAGAGTGGAAATTTAAAAATGTTTAGATGAAA 1095
Db 594 TTGAAAAAATGGGAATTTCTCAGCGCTTTGTGAGTGAATATAAAACATCCTCGGATGG 653
QY 1096 CATACAGATGTTGGGTGGAACGAGATGAGCAAAATATTCATGATGTTGTAACATGTCCTT 1155
Db 654 CATACAAATTTGCTGGTTTACAGAAAGATGAGGAATCATGATGGACATAGCAACATTTGCNA 713
QY 1156 TAGCCTTTCGGTTTATTAAGGATCAATGGGTATGAAGTTTCCCAGATCCATTTGGCTGAAA 1215
Db 714 TGGCATTCNCCTTTTGGANGATGANTGGTTTCAATGTTTCTCCTCNGAIGANTCTGTCTCAGC 773
QY 1216 TTACTAATGAATTAGCTTTGAAAAGA 1240
Db 774 TTGCTGGANCTTCCACTTTCCATGA 798
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RESULT 5
US-09-398-395A-55
; Sequence 55, Application US/09398395A
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; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468721, Joseph P.
; APPLICANT: Starke, Courtney R.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-398-395A-55

Query Match          7.0%; Score 194.8; DB 3; Length 2861;
Best Local Similarity 47.8%; Pred. No. 6.8e-40;
Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

QY 337 ATGTAGAAATTTCTGTTCTTCATATGACACACATGGGTAGCCATGGTCCCTTCCTCAA 396
DB 397 ATGGCGAAACGAATCCCTCTGCGATATGACATGCTGTTGGGTAGCAAGGATCCAGCATG 456

QY 397 ACTCACCAATCGCCTGTTTCCCTGAGTGTCTCAATGGTTAAATTAATAATCAGCTTA 456
DB 457 ATGGCTCTGACACCCCTCACTTCTCTGAGCGGTGATGATGATCTTCAAAATCAGTTGA 516

QY 457 ATGATGTTTCATGGGTCCTGTTTAATCACAATCAATCAATCAATCAATCAATCAATCA 516
DB 517 AAGATGGGTCTGGGGTGAAGGATCTTACTTC-----TTGCCATATG 558

QY 517 ATTCTCTATCTTCAACATTAAGCATGATTTGTCATTAATAAAGATGGAATGTTGGGAAG 576
DB 559 ACAGAAATACCTGGTACATCTGCAATGATTAATTAATTAATTAATTAATTAATTAATTA 618

QY 577 ATCAATAATAAAGGTCTAAGTTTATTTAGTCAAAATCTTGCTTCAGCTACTGAAATAAA 636
DB 619 CACAGTACAGAAAGGTATTTGAATTTCTTACAGACACAGCTGGAAGATGGAAGTGAAG 678

QY 637 GTCACCAATCT---CCATTTGGTTTGACATCATATTTCTCTGTTGTTGCTTTGAGTATGCGA 693
DB 679 CTGATAGTCTAGGCCAAGTGGATTTGAAATAGTATTTCTGCAATGCTTAAGAGAGCTA 738

QY 694 AAACTTGGACATAAACCCTCTTTCAAAACACAGATTTTATTTGATGATGCTACATAAGA 753
DB 739 AAATCTTAGGCTTTGGATCTGCTCTTACGATTTGCAATTTCTTGAACCAATCATCGAAAGC 798

QY 754 GCGAATTTGGAGCAAAAGATGCCATTAATGAGATGGAATG-----GATACTGG 804
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QY 805 CGTATATCTCTGAAGGACTCGGTAATTTATATGATTTGGAATATGGTGAAGAAATATCAGA 864
DB 859 TGTATTTCTTTGGAAGGTTTACAGAAATAGTAGACTGGCAGAAAAATAATGAAACTTCAAT 918

QY 865 TGAATAATGTTCTGTTTTCACCTCACCATCAGCAACAGCTGCTGCTTCAATTAATCATC 924
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QY 925 AAAATCTGCTGCTTAAATTAATTAATTTCACTTTTGGACAAAGTTTGGTAAATGCAGTCC 984

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DB 979 GGAACAAAAGTGTCTTGAACCTTTGCTTGAAGAAATTCGGAACCAATGTC 1038
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QY 1105 GTTGGGTGGAACGAG-----ATGAGCAAAATATTATCATCGATGTTTGAACAT 1149
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Qy 2071 GCCCGATTGT 2080

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RESULT 6

US-09-887-586A-55

; Sequence 55, Application US/09887586A

; Patent No. 6495354

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. 64953541, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/887,586A

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 55

; LENGTH: 2861

; TYPE: DNA

; ORGANISM: Abies grandis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3)...(2606)

; OTHER INFORMATION: abietadiene synthase

US-09-887-586A-55

Query Match 7.0%; Score 194.8; DB 3; Length 2861;

Best Local Similarity 47.8%; Pred. No. 6.8e-40;

Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

Qy 337 ATGTAGAAATTTCTGTTTCTTCATATGACACAGCATGGGTAGCATGGTCCCTTCTCCAA 396

Db 397 ATGGCGAAACGAATCCCTCTGCATATGACACTGCTTGGGTAGCAAGGATCCAGCGTTTG 456

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Qy 577 ATCAATAATAAAGGTCTAAGTTTATTGAGTCAAAATCTTGCTTCAGCTACTGAAAAAA 636

Db 619 CACAGTACAGAAAGTATTGAATCTTCAGACACAAGCTGGAAGATGGAAGATGAAG 678

Qy 637 GTCAACCACTCT---CCCATTTGTTGACATCATATTTCTGTTTGTGATGATGCGA 693

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Db 1399 TGAAGAGAGCAAACTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAATAATGTCGATG 1458

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Db 1579 CAGATGATGTGGCTTGGAAAACTGTATATATGATGCATACATTTCCGAATGAAAGAT 1638

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 1879 CCCATGGATCTTTAGACGATCTTAAGTTGTTTCACAGAAATCAGTCAAAAGATGGGATCTAT 1938
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RESULT 7

US-09-895-752-55
 ; Sequence 55, Application US/09895752
 ; Patent No. 6559297
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 6559297, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/895,752
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 09/398,395
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: Fast-Seq for Windows Version 3.0
 ; SEQ ID NO 55
 ; LENGTH: 2861
 ; TYPE: DNA
 ; ORGANISM: Abies grandis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (3)...(2606)
 ; OTHER INFORMATION: abietadiene synthase
 US-09-895-752-55

Query Match 7.0%; Score 194.8; DB 3; Length 2861;
 Best Local Similarity 47.8%; Pred. No. 6.8e-40;
 Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

337 ATGTAGAAATTTCTTCTTCATATGACAGCATGGGTAGCCATGGTCCCTTCTCCAA 396
 397 ATGGCGAAACGAATCCCTCTGTCATATGACATGCTGTTGGGTAGCAAGGATTCAGAGCATG 456
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QY 2071 GCCCGATTGT 2080
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RESULT 8

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US-09-903-012B-55
; Sequence 55, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-903-012B-55

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Query Match 7.0%; Score 194.8; DB 3; Length 2861;

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Best Local Similarity 47.8%; Pred. No. 6.8e-40;
Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

QY 337 ATGTAGAAATTTCTGTTTTCATATGACACAGCATGGGTAGCCATGGTCTCTTCTCCAA 396
Db 397 ATGGCGAAACGAATCCCTCTGCAATGACACTGCTGGGTAGCAAGATTCACGACGATTG 456
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QY 985 CAACAGTTTATCTCATGATTTTATTCGCACTTTCTATGTTGACACAAATTTGAAGAT 1044
Db 1039 CTTGTCACTATCCGCTTGATCTATTTGAACGTTTGTGGCGGTTGATACAGTTGACGGC 1098
QY 1045 TAGGAATTTACACCACTTTACAGATGGAAATTAAGAAATGTTTGTAGATGAACATACAGAT 1104
Db 1099 TAGGTATCGATCGTCATTTCAAAGAGGAGATCAAGGAAGCAATTTGGATTTATGTTTACAG 1158
QY 1105 GTTGGGTGGAACGAG-----ATGACCAATATATTCATGATGTTGTAACAT 1149
Db 1159 ATTGGGACGAAAGAGGCAATTTGGATGGCGAGAGAGAAATCCTGTTCTGATATTTGATGATA 1218
QY 1150 GTGCTTTTAGCCTTTTCGGTTTATTAAGGATCAATGGGTATGAAGTTTCCCGAGATCCATGG 1209
Db 1219 CAGCCATGGCCCTTCGAATCTTGAGATTCATGATGATACATGTAATCTCAGATGTTTAA 1278
QY 1210 CTGAAATTAATGAATTTAGCTTTTGAAGACGAATATGCAAGCTCTTTGAAACATATCATG 1269
Db 1279 AAAATTTAGAGATGAGAAATGGGAGTTCTTTTGTCTTCTTGGGTCAAAACACAGAGAGGAG 1338
QY 1270 CGTCACATATATATACC-----AAGAGATTTATCTTCTGGAACAAATCT 1317
Db 1339 TTACAGACATGTTAAACGTCGAATCGTTGTTCATGTTTCAATTTCCGGGAGAAACCATCA 1398
QY 1318 TGAAGTCAGCTGATTTTC-----CTCAAAGAGATAATAT 1350

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Db 1399 TGAAGAAGCAAACTCTGTACGAAAGGTATCTGAGAAATGCTCTGGAATAATGTGGATG 1458
Qy 1351 CCACGTGATTCACACAGGCTTCTAAATTAATTCACAAAGAGGTGGAATAATGCTCTTAAGT 1410
Db 1459 CTTTGGCAATGGCTTTTAAAGAAATATTCGGGAGAGGTAGAGTATGCACTCAAT 1518
Qy 1411 TCCCTATCAATACCGGTTTGAACGCAATAACACATAGACGAAATATACAGCTTTTACAATG 1470
Db 1519 ATCCCTGGCATAGAGTATGCAAGGTGGAGGCTAGAGCTATATTTGAAACATATGGGC 1578
Qy 1471 TAGCAATACAGAAATTTCTGAAACTACATATCACTCATCAATATTTAGTAACACTGATT 1530
Db 1579 CAGATGATGTGTGGCTTTGGAATAACTGTATATATGATGCCATACATTTGCAATGAAAGT 1638
Qy 1531 ACCTAAGGTTGGCTGTTGGAAGATTTCTACACCTGCCAATCTATTATTCGTGGAAGATTAA 1590
Db 1639 ATTGAACTAGCGAACTGCACTTCAATAAGGTGCACTATACACCAACAGAGCTTC 1698
Qy 1591 AAGGCTTTGAAGGTGGGTGAGAGAAATAGTTGGACCAAGCTCAAGTTTGTAGGCAAA 1650
Db 1699 AAGATCTTCGAAGGTGGTGAATCATCCGGTTTTCACGGATCTGAAATTCACCTGCGAGC 1758
Qy 1651 AGACCGCTACTGTATTTCTCTGCTGCTGCAACACTTTCTGCTCCGAATTAATCAGATG 1710
Db 1759 GTGTGACGGAATATATTTCTCACCGCATCTTTATCTTTGAGCCGAGTTTCTAAGT 1818
Qy 1711 CGGTATTTTCATGGGCCAAATAAGGCAATTAACACAGTAGTTGATGACTTTTGTGATA 1770
Db 1819 GCAGAGAGTTTATACAAAACTTCCAAATTTCACTGTTATTTTAGATGATCTTTATGACG 1878
Qy 1771 TCGGTGTACAACTCGATGAATTTGACCAACCTGATTCAAATGTGTTGAAAAATGGAATGAG 1830
Db 1879 CCATGATCTTTAGAGCATCTTAAGTTGTTTCAGAAATCAGTCANAAGATGGATCTAT 1938
Qy 1831 ATGTGCAAGAGATGTTGTTTCAGAGCATGTTGCGATTTTATTTTACAGATTTAAAGATG 1890
Db 1939 CACTAG---TGGACCAATGCCAACAAATGAAATATGTTTGTGGGTTTCTACAATA 1995
Qy 1891 CAATCTGTGGATGGAGATGAGCTTTTAAATGGCAAGCGCGAGTAACTAGCCATG 1950
Db 1996 CTTTAAATGATATAGCAAAAGAGGACGTGAGAGGCAAGGCGCGATGTGCTAGGCTACA 2055
Qy 1951 TTAATCAAACTGGTTGGAACTAATGAATAGTATGTTGAGAGAGCTATATGGACAAAG 2010
Db 2056 TTCAAAATGTTGGAAGTCCAACTTGAAGCTTACACGAAGAGAGAGATGTTCTGAAG 2115
Qy 2011 ATGCTTATGTCACCAATTAATGAATATATGGAATAACGCTTACGTGCTATTTGCAATG 2070
Db 2116 CTAATATGTGCCATCTTCAATGAATACATAGAGATGCGAGTGTGTCAATAGCATTGG 2175
Qy 2071 GCGCGATTGT 2080
Db 2176 GAACAGTCGT 2185

RESULT 9

US-09-900-797-55

; Sequence 55, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6645762, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-900-797-55

Query Match 7.0%; Score 194.8; DB 3; Length 2861;
Best Local Similarity 47.8%; Pred. No. 6.8e-40;
Matches 866; Conservative 0; Mismatches 857; Indels 87; Gaps 7;

Qy 337 ATGTAGAAATTTCTGTTTCTTATATGACACAGCATGGGTAGCCATGGTCCCTTCTCAA 396
Db 397 ATGGCGAAACGAATCCCTCTGCATATGACACATGCTTGGGTAGCAAGGATTCAGCAGTTG 456
Qy 397 ACTCACCCAAATCGCCTTGTTCCTGAGTGTCTCAATGGTTAATTAATAACAGCTTA 456
Db 457 ATGGCTTGACAAACCTCACTTTCTGAGACGGTTGAATGGAATCTTCAAAATCAGTTGA 516
Qy 457 ATGATGGTTTCATGGGCTTGTGTTAAATCACACTATAATCAATCACCCGTGCTTAAAG 516
Db 517 AAGTGGGCTTGGGGTGAAGGATTTCTACTTC-----TTGGCATATG 558
Qy 517 ATTCTCTATCTTCAACATTAGCATGATTTGTTGCATTTAAAGATGGAATGTTGGGGAAG 576
Db 559 ACAGAATACTGGCTACACTTGCATGATTTATTATACCTTACCTCTGGCGTACTGGGAGA 618
Qy 577 ATCAATAATAAAGTCTAAGTTTATTGAGTCAATCTTGGTCTGAGTCTAGCTACTGAAAAA 636
Db 619 CACAGGTACAGAAAGTATTGAATTTCTTCAGSACACAGCTGGAAGATGGAAGATGAAG 678
Qy 637 GTCAACCATCT---CCATTGGTTTGAACATATTTCTGTTGTTGCTTGTGATGATCGGA 693
Db 679 CTGATAGTCATAGGCCAAGTGGATTTGAATAGTATTTCTGCAATGCTAAGGAAGCTA 738
Qy 694 AAAAATTGGACATAAACCTCTTCAAAAACAAACAGATTTTGTGATGATGCTACATAGA 753
Db 739 AAATCTTAGGCTTGGATCTGCTTACGATTTGCAATTTCTTGAACAAATCATCGAAAGC 798
Qy 754 GGAATTTGGAGCAAAAAGATGCCATTCAATGAGATGAGT-----GATACTGG 804
Db 799 GGGAGGCTAAGCTTAAAGGATTTCCCACTGATGTTCTCTATGCCCCTTCCAAACACGTTAT 858
Qy 805 CGTATATCTCTGAAGGACTCGGTAATTTATATGATTTGGAATATGTTGAAGAAATATCAGA 864
Db 859 TGTATTTCTTGGAAAGGTTTACAAGAAATAGTAGCTGGCAGAAATATGAAACTTCAAT 918
Qy 865 TGAATAATGTTCTGTTTCACTCACCATCAGCAACAGCTGCTGCTTTCATTAATCATC 924
Db 919 CCAAGGATGATCATTTCTCAGCTCTCCGSCATCTACAGCGGCTGATTTATCATGCGTACAG 978
Qy 925 AAAATCCTGGTGTCTTAATTTAAATTCATTTTGGACAAAGTTTGGTAATGCACTCC 984
Db 979 GGAACAAAAAGTCTTGGATTTCTTGAACATTTCTTGAAGAAATTCGGAACCAATGTC 1038
Qy 985 CAACAGTTTATCTCATGATTTTATTTATCCGACTTTCTATGTTGACACAAATTTGAAAGAT 1044
Db 1039 CTTGTCACTATCCGCTGATCTATTTTGAAGCTTTTGGGCGGTTGATACAGTTGAGCGGC 1098
Qy 1045 TAGGAATTTTACACCACTTTTCAAGAGTGGAAATTTAAAAATTTTAGATGAAACATACAGAT 1104
Db 1099 TAGGTATCGATCGTCAATTTCAAGAGGAGATCAAGGAAGCATTTGGATTATGTTTACAGCC 1158
Qy 1105 GTTGGGTGGAAACGAG-----ATGAGCAAAATTTATCATGAGTGTGTAACAT 1149
Db 1159 ATTGGGACGAAAGAGGCAATTTGGATGGCGGAGAGAAATCTGTTCTCTGATATTGATGATA 1218

QY 865 TGAATAATGGTCTGTTTCAACTCACCATCAGCAGCTGCTCTTTCAATTAATCATC 924
 Db 919 CCAAGGATGGATCATTTCTCAGCTCTCCGGCATCTACAGCGGCTGATTTCAATCGGTACAG 978
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 Db 1039 CTTGTCACTATCGCTGTGATCTAATTTGAACGTTTGTGGCGGTTGATACAGTTGAGCGC 1098
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 Db 1099 TAGGTATCGATCGTCAATTTTCAAGAGGAGATCAAGGAAGCATTTGGATTTATTTTACAGCC 1158
 QY 1105 GTTGGGTGGAACGAG-----ATGACCAATATTTCAATGGATTTGTAACAT 1149
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 QY 1150 GTGCTTTAGCTTTTCGGTTTATTAAGGATCAATGGGTATGAAGTTTCCCGAGATCCATGG 1209
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 QY 1210 CTGAAATTTACTAATGAATTTAGCTTTGAAAGCAATATGCACTCTTGAAACATATCATG 1269
 Db 1279 AAACATTTAGAGATGAGATGGGGAGTTCTTTTGTCTTCTGGGTCAAAACACAGAGAGGAG 1338
 QY 1270 CGTCAATATTTATATACC-----AAGAGGATTTATCTCTGGAAACAAATCT 1317
 Db 1339 TTACAGACATTTAAACGTCATTCGTTGTTTCAATGTTTCAATGTTTCGGGAGAAACGATCA 1398
 QY 1318 TGAAGTCAGCTGATTTTC-----CTCAAGAGATAAAT 1350
 Db 1399 TGAAGAACGAAACTCTGACGAAAGTATCTGAGGAATGCTCTGGAATAATGCGATG 1458
 QY 1351 CCACTGATTTCAACAGGCTTTCTAAATTAATTTCAAGAGGTGGAAATGCTCTTAAGT 1410
 Db 1459 CTTTGACAAATGGGCTTTTAAAGAAATTTTCGGGAGAGGTAGAGTATGCACACTCAAT 1518
 QY 1411 TCCTATCAATACCGGTTTGAAGCAATAAACACTAGACGAAATATACAGCTTTTACAATG 1470
 Db 1519 ATCCCTGGCATAGAGATGCGGAGGTGGAGGCTAGAGCTATATTTGAAACTATGGGC 1578
 QY 1471 TAGACAAATCAAGAATTTCTGAAACTACATATCACTCATCAATATTAATTAAGTAACTGAT 1530
 Db 1579 CAGATGATGTTGGCTTTGAAAGAACTGTATATATGATGCAATACATTTTCGAATGAAAGT 1638
 QY 1531 ACCTAAGGTTGCTGTTGAAGATTTCTACACCTGCCAATCTATTTATCTGTAAGAAATTA 1590
 Db 1639 ATTAGAATCTAGCGAAACTGGACTTCAATAAGGTGCACTCTACACCAACAGAGCTTC 1698
 QY 1591 AAGGCTCTGAAAGTGGGTGAGAAATAAGTTGACACGCTCAAGTTTGTCTAGGCAAA 1650
 Db 1699 AGATCTTGAAGGTGGTGAATCATCCGTTTACGGATCTGAATTTTCACTCTGAGC 1758
 QY 1651 AGACCGCTACTGTTATTTCTCTGTTGCTGCAACACTTTTCGTCCTCCGAAATATCAGATG 1710
 Db 1759 GTGTGACGGAATATATTTCTCACCGGCATCTTTATCTTTGAGCCGAGTTTCTAAGT 1818
 QY 1711 CGGTAATTTCAAGGCGCAAAATGGAATTAATTAAGTATGATGATGATGATGATGATGATGAT 1770
 Db 1819 GCAGAGAGGTTTATACAAAACCTTCACTGTTATTTTATGATGATGATGATGATGATGATGAT 1878
 QY 1771 TCGGTGTTCAATTCGATGATTTGACCAACTGATTTCAATGTTGTTGAAATAAGAAATGATG 1830
 Db 1879 CCATGATCTTTAGACGATCTTTAAGTTGTTACAGAACTGATCAAGAAAGATGGATCTAT 1938
 QY 1831 ATGTGACAAAGGATTTGTTTACAGACATGTTTCGGATTTTATTTTATGATTTTAAAGATG 1890
 Db 1939 CACTAG---TGGACCAAAATGCCCAAAATGAATATGTTTGTGGGTTTCTACAATA 1995
 QY 1891 CAATCTGTTGGATTTGAGATGAAGCTTTTAAATGGCAAGCGCGGATGTAACCTAGCCATG 1950

Db 1996 CTTTAAATGATATAGAAAAGAGGACGTGAGAGGCAAGGGCGGATGCTAGGCTACA 2055
 QY 1951 TTATTCAAACTTTGGTTGGAACTAAATGAATAGTATGTTGAGAGAAGCTATATGCAAGAG 2010
 Db 2056 TTTCAAAATGTTTGGAAAGTCCAACCTTGAAGCTTACACGAAAGAGCAGAAATGCTCTGAAG 2115
 QY 2011 ATGCTTATGTCGCAACATTTAAATGAATATATATGGAACCCCTTACGTTGCTCAATTTGCAATTAG 2070
 Db 2116 CTTAAATATGTCATCTCTTCAATGAATACATAGAGAATCGAGTGTGTCAATAGCAATTGG 2175
 QY 2071 GCCCGATTCT 2080
 Db 2176 GAACAGTCTG 2185

RESULT 12
 US-09-315-861-1
 ; Sequence 1, Application US/09315861
 ; Patent No. 6114160
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodney B. Croteau, Mark R. Wildung
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TAXOL
 ; TITLE OF INVENTION: BIOSYNTHESIS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Donald L. Stephens Jr.
 ; STREET: One World Trade Center
 ; STREET: 121 S.W. Salmon Street
 ; STREET: Suite 1600
 ; CITY: Portland
 ; STATE: Oregon
 ; COUNTRY: United States of America
 ; ZIP: 97204
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3-1/2 inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/315,861
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/843,363
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Donald L. Stephens Jr.
 ; REGISTRATION NUMBER: 34,022
 ; REFERENCE/DOCKET NUMBER: 4630-46842/DLS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2700 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double stranded
 ; TOPOLOGY: linear
 ; US-09-315-861-1

Query Match 5.5%; Score 153.8; DB 3; Length 2700;
 Best Local Similarity 46.7%; Pred. No. 2.5e-29;
 Matches 943; Conservative 0; Mismatches 992; Indels 84; Gaps 11;
 QY 335 AAATGTAGAAATTTCTGTTTCTTCAATGACACAGCATGGTAGCCATGCT-----CCC 388
 Db 414 AGACGAGATATGATGCTCGTCTGCATACGACTGCTGGTGGCGAGGCTGGCGACCAT 473
 QY 389 TTCTCCAAACTCACCCAAATCGCCTTGTTCCTCGATGCTCAATGTTGTTAATTAATAA 448
 Db 474 TTCTCTGATGATCTGAGAAGCCAGGTTTCTCTAGGCCCTCAACTGGGTTTCAACAA 533


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; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Taxus brevifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)....(2607)
; OTHER INFORMATION: taxadiene synthase
US-09-398-395A-43

Query Match      5.5%; Score 153.8; DB 3; Length 2700;
Best Local Similarity 46.7%; Pred. No. 2.5e-29;
Matches 943; Conservative 0; Mismatches 992; Indels 84; Gaps 11;

QY 335 AAATGTAGAAATTCCTGTTCTTCATATGACACAGCATGGGTAGCCATGGT-----CCC 388
DB 414 AGACGGAGATATCAGTCCGCTGTCATACGACATCGCGTGGGTGGCGAGCTGGCGACCAT 473
QY 389 TTCTCCAAACTCACCCTGCTGTTTCCCTGAGTGTCTCAATGGTAAATTAATAA 448
DB 474 TTCTCTGATGATCTGAGAGCCAGGTTTCTCAGGCCCTCAACTGGGTTTCAACAA 533
QY 449 TCAGCTTAATGATGGTTTCATGGGCTTGTAAATCACTCATATATCAATCAATCAACCCGTT 508
DB 534 CCAGCTCCAGGATGGATCGTGGGGTATCGAATCGCACCTTTAGTTTATGGATCGATTGCT 593
QY 509 GCTTAAGATTCCTATCTCTACATATAGCATGATTTGTTGCAATTAAGATGGAATGT 568
DB 594 -----TAACACGACCAATCTGTATCGCCCTCTCGGTTTGGAAAC 635
QY 569 TGGGGAAGATCAATAAATAAGGTCTAAGTTTATTGAGTCAAAATCTTGTCTCAGCTAC 628
DB 636 AGGCGACACCCAGTACACAGGTGCTGAGTTTATTGACAGATCTAAGATTAATCTCAA 695
QY 629 TGAATAAGTCAACCATCTCCATGGTTTGGACATCATATTTCTCTGGTTTCTGTGAGTA 688
DB 696 TGAGGAAGATGATGTGCTCC-----GGATTCCAAATAAATCTTCTCTGCTCTGCTGCAAA 752
QY 689 TCGGAAAACTTGGACATAAATCTCTTTCAAAACAAACAGATTTTGTGATGCTACA 748
DB 753 GGCATAAGCGTTGGGGATCAATCTTCTTACGATCTTCCATTTATCAAAATATTTGTCGAC 812
QY 749 TAAGAGGGAATGGAGCAAAAAGATGCCAT-----TCAAAATGAGATGGATGATCTT 802
DB 813 AACACGGGAAGCCAGGCTTACAGATGTTTCTGCGGCAGCAGACAAATATTCAGCCAAAT 872
QY 803 GCGGTATATCTCTGAAGGACTCGGTAATTTATATGATGGAATATGGTGAAGAAATATCA 862
DB 873 GTTGAATGCGTTGGAAGGCTCGAGGAAGTATTGACTGGAAACAGATTTATGAGGTTTCA 932
QY 863 GATGAAAAATGTTCTGTTTTCATCCACCATCAGCAACAGCTGCTCTTCAATTAATCA 922
DB 933 AAGTAAGATGATGATTTCTCTGAGCTCCCTGCTCCACTGCTGTGTACTGATGAATAC 992
QY 923 TCAAAATCTGTTGTCTTAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 982
DB 993 AGGGGACGAAATAATGTTTACATTTTCTCAACATCTGCTCGACAAATTCGGCGGCTGCT 1052
QY 983 CCCAACAGATTTATCCATGATTTATTTATCCGACTTTCTATGGTTGACACAAATTTGAAG 1042
DB 1053 GCCCTGTATGATTTCCATCGATCTGCTGGAACGCCCTTTCGCTGTTGTAATAATGAGCA 1112
QY 1043 ATTAGAAATTTACACCAATTTTCAAGTGGAAATTAATAATTTTATAGATGAACATACAG 1102
DB 1113 TCTCGGAATCGGTGCGCATTTCAACAAAGAAATCAAAAGAGCTCTTGTATGTCTACAG 1172
QY 1103 ATGTTGGGTGGAACGAG-----ATGAGCAAAATATTCAATGGATGTTGTAAC 1147
DB 1173 ACATTTGAGTGAAGGGGATCGGTTGGGCGAGAGACGCTTGTTCAGATCTCAACAC 1232
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QY 1148 ATGTGCTTTAGCCTTTCGGTTATTAAAGGATCAATGGGTATGAAGTTTCCCGAGATCCATT 1207
DB 1233 CACAGCCCTCGCCCTCGCGAACTCTTTCGCATGCACGGATCAATGTTTCTCAGACGTTTT 1292
QY 1208 GGCCTGAAATTTACTAATTAATTAAGTTTGAAGACGAATATGCAGCTC----- 1254
DB 1293 GAATTAATTTCAAGATGAAGAACGGGGGTTCTTCTCTCTGCGGCGCAACCCATGTCGA 1352
QY 1255 -TTGAAACATATCATCGGTCACATATATTTATACCAAGA--GGATTTATCTTCTGGAAAAAC 1311
DB 1353 ATTGAGAGCGGTGGTGAATCTTTTTCAGAGCTTCCGACCTTGCATTTCTCTGACGAAAGAGC 1412
QY 1312 AAATCTTGAAGTCAGCTGATTTTCTCAAGAGATTAATATCCACTGATTTCAACAGCGCTTT 1371
DB 1413 TATGGACGATGCTGAAATAATTTGCAAGACCAATATCTTAGAGAGGCACTTTGCAACGAAAT 1472
QY 1372 CTAAATTAATTTCA-----CAAGAGGTGAAATGCTCTTAAGTTCCCTTATCAATAC 1423
DB 1473 CTCACCAATACAAACATTAATCAAGAGATTGAGTACGTGGGTGGAGTACCTTGGCACAT 1532
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DB 1533 GAGTATCCACGCTTAGAAGCCAGAAAGTTATATGATTCTATATGACGACAAATTTATGATG 1592
QY 1484 AATCTCTGAATACTCATATCATCTCATCAATATTAGTAACTGATTAAGTAAAGTTGGC 1543
DB 1593 GCAGAGGAGAGCTCTATATAGAATGCCATCTTTGAGTAAATCAAAATGTTTGAATTTGC 1652
QY 1544 TGTGGAAGATTTCTACACCTGCAATCTATTTATCTGTAAGAAATTTAAAGGCTCTTCAAG 1603
DB 1653 AAAATTTGACTTCAATATCGTACATCTTTGATCAAGAGGAGTTGAGCTTTCTAACAAG 1712
QY 1604 GTGGGTGTGAGAGAATAAGTTGGACCCAGCTCAAGTTTGTAGCGCAAAAAGACCGCTTACTG 1663
DB 1713 ATGGTGAAGGAATCCGGCATGGCAGATATAAATTTCACTCGCACCCGAGTGGCGAGGT 1772
QY 1664 TTATTTCTCTGTTGCTGCAACACTTTGCTCTCCGAAATTTATCAGATGCGGCTATTTCTATG 1723
DB 1773 TTATTTTCTCATCAGCTACA-----TTTGAACCCGAAATATCTGCCACTTAGAATTTGCC 1826
QY 1724 GGCCTAAAATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1783
DB 1827 CACAAAAATTTGTTGTTTCAAGTCTTTTCAAGTATGATGCTGACATCTTTGCAACACT 1886
QY 1784 CGATGAATTTGACCAACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1843
DB 1887 AGATGAATTTGAAAGTCTTCACTGAGGAGTAAAGAGATGGGATACATCTTTGCTACATGA 1946
QY 1844 TTGTTGTTTCAAGACATGTTCCGATTTTATTTTATTTAGCATTTAAAGATGCAATCTGTTGGAT 1903
DB 1947 ---GATTCAGAGTGTATGCAAACTTGTCTTTAAAGTTTGGTTTCAAAATTAATGGAAGAAT 2003
QY 1904 TGGAGATGAAGCTTTTAAATGGAAGCGCGCATGTAACTAGCATGTTTATTTCAAACTTTG 1963
DB 2004 AAATTAATGATGTTTAAAGTACAGAGCTGACATGCTGCTCACAATGAAGAAACCTTG 2063
QY 1964 GTTGAACCTTAATGAATAGTATGTTGAGAGAACTATATGGAACAAGATGCTTTATGTGCC 2023
DB 2064 GGAGTTGTTACTTCAATTTGTTATGTAACAAGAAAGGAGTGGCTTGAAGCCGGGTATATACC 2123
QY 2024 AACATTAATGAATATATGGAATAACGCTTACGTTGATTTTGTGATTTAGGCGCGATTTGTCAA 2083
DB 2124 AACTTTTGAAGAGTACTTTAAAGACTTATGCTATATCAGTAGGCTTTGGACCGGTGTACCT 2183
QY 2084 GCGGCTATTTACTTTTGTGGGCCCCAAATTTATCAGAGGAGATTTGTTGAAAGCTCTGAATA 2143
DB 2184 ACAACCAATCTACTAATGAGGAGCTTGTGAAAGATGATGTTTGTGAGAAAGTGCACATA 2243
QY 2144 TC---ATAATCTATTAAAGTAAATGAGCAGCGGTCGACTTCTTAAACGATATATCCATAG 2200
DB 2244 TCCCTCAATAATGTTTGTAGCTTGTATCTTTGAGCTGGCGACTAAACAAACGACACCAAAAC 2303
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Qy	2201	CTTCAAGAGGAA	TTAAGNAGCAAT	TAAACGCGTAGCAT	TTCATTTGAGTAACGG	2260
Db	2304	ATATCAGGCTG	AAAAAGGCTC	GAGGACAAACAA	AGCCCTCAGGCATAGCAT	2363
Qy	2261	AGAAAGTGGGA	AGTGGGAAGAGG	TTGTGGAGGAGAT		2299
Db	2364	TAATCCAGGAG	CACTGAGAAGAT	GCCATTTAAGCACAT		2402

RESULT 14

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US-09-887-586A-43
; Sequence 43, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Taxus brevifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(2607)
; OTHER INFORMATION: taxadiene synthase
US-09-887-586A-43

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Query Match	5.5%	Score 153.8;	DB 3;	Length 2700;
Best Local Similarity	46.7%	Pred. No. 2.5e-29;		
Matches 943;	Conservative	0;	Mismatches 992;	Indels 84;
				Gaps 11;

335	Qy	AAATGTAGAAATTTCTGTTTCTTCATATGACACAGCATGGGTAGCCATGTT-----CCC	388
389	Qy	TTCTCCAAACTCACCCAAATGCGCTTGTTCCTCGAGTGTCTCAATTGGTTTAATATAA	448
414	Db	AGACGGAGATATCAGTCGGTCTGCATACGACACTCGCTGGGTGGCGAGGCTGGCGACCAT	473
474	Db	TTCTCTGTATGATCTGAGAAGCACCGGTTTCCTCAGCGCCCTCACTGGGTTTTTCAACAA	533
449	Qy	TCAGCTTAATGATGGTTCATGGGGTCTTGTTTAATCACACTCATTAATCATTAATCACCCGTT	508
534	Db	CCAGCTCCAGATGGATCGTGGGGTATCGAATCGCACTTTAGTTTATGCGATCGATTGCT	593
509	Qy	GCITTAAGATTCTCTATCTTCAAATTTAGCATGTATTGTTGCATTAAGAGATGGATGT	568
594	Db	-----TAAACGAGCCAAATCTTGTTATCGCCCTCTCGGTTTGGAAAC	635
569	Qy	TGGGAGATCAATAATAAAGCTCTAAGTTTTATTGAGTCAAACTCTGCTCAGCTAC	628
636	Db	AGGGCACAGCCCAAGTACAACAAGGTGCTGAGTTTTATTGCGAGAGAACTTAAGATTACTCAA	695
629	Qy	TGAAAAAGTCAACCATCTCCCATGGTTTTGACATCATATTTCTCGTTTGCCTTGAGTA	688
696	Db	TGAGGAAGATGAGTTGTCCTCC-----GGATTTCCAAATAATCTTTTCTGCTCTGCTGCAAAA	752
689	Qy	TGCGAAAAAATTGGACATAAACCTCTTTTCAAAAAACAAAGATTTTAGTTTGATGCTACA	748
753	Db	GGCAAAAGCGTTGGGGATCAATCTTCTCTAGCATCTTCCATTTATCAATAATTTGTGCAC	812
749	Qy	TAAGAGGGAAATTGGAGCAAAAAAGATGCCAT-----TCAAATGAGATGGATGGATACTT	802

Db 1887 AGATGAATTCAGAAAGTTTCACTCAGGAGTAAGAGATGGGATACATCATCTTTGCTACATGA 1946
 QY 1844 TTGTTGTCAGAGCATGTTTCGGATTTTATTTTATGCAATTAAGAGATGCAATCTGTTGGAT 1903
 Db 1947 ---GATTCAGAGTGATGCAAACTTGTCTTAAAGTTTGTTCCTCAAAATTAATGGAAGAGT 2003
 QY 1904 TGGAGATGAAGCTTTTAAATGGCAGCGCGGATGTAACATAGCCATGTTTATTCAAACTTG 1963
 Db 2004 AAATAATGATGTGGTTAAAGGTACAAGGACGTGACATGCTCGCTCACATAAGAAAACCTG 2063
 QY 1964 GTTGGAACTAAATGAATAGTATGTTGAGAGAGCTATATGACACAAGAGATGCTTATGTGCC 2023
 Db 2064 GAGTTGTACTCAATGTTATGTAACAAGAGGAGTGGCTTGAAGCGGGTATATACC 2123
 QY 2024 AACATTAATGAATATATGAAACCGCTTACGTTGCTCAATTTGCAATTAGGCCCGATGTCAA 2083
 Db 2124 AACTTTTGAAGAGTACTTAAAGACTTATGCTATATCAGTAGGCTTTGGACCGTGTAACCT 2183
 QY 2084 GCGGCTATTTACTTGTGCGGCCCAAAATATATCAGAGGAGATGTTTGAAGCTCTGAATA 2143
 Db 2184 ACAACCAATFACTAATCGGTGAGCTTGTGAAAGATGATGTTGTTGAGAAAAGTGCACTA 2243
 QY 2144 TC---ATAATCTATTAAGCTAATGAGCAGCAGCGGTCCGACTTCTAAACGATATCCATAG 2200
 Db 2244 TCCTCAATATGTTTGACCTTGATCTCTTGAGCTGGCGACTAAACAAGCACCAAAAC 2303
 QY 2201 CTTCAAGAGGGAATTTAAGAGAGGCAAAATTAACCGCGTAGCATTTGAGTTAAACGG 2260
 Db 2304 ATATCAGGCTGAAAGGCTCGAGGACACAAGCCTCAGGCATAGCATGCTATATGAAGCA 2363
 QY 2261 AGAAGTGGAAAGTGAAGAGAGAGTGTGAGGAGAT 2299
 Db 2364 TAATCAGGAGCAACTGAGGAGATGCCATTAAGCACAT 2402

RESULT 15

US-09-895-752-43
 ; Sequence 43, Application US/09895752
 ; Patent No. 6559297
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. 6559297, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/895,752
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 09/398,395
 ; PRIOR FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/100,993
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 43
 ; LENGTH: 2700
 ; TYPE: DNA
 ; ORGANISM: Taxus brevifolia
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (22)...(2607)
 ; OTHER INFORMATION: taxadiene synthase
 US-09-895-752-43

Query Match 5.5%; Score 153.8; DB 3; Length 2700;
 Best Local Similarity 46.7%; Pred. No. 2.5e-29;
 Matches 943; Conservative 0; Mismatches 992; Indels 84; Gaps 11;
 QY 335 AAATGTAGAAATTTCTGTTCTTCATATGACACAGCATGGTAGCCATGCT-----CCC 388

Db 414 AGACGAGATATCAGTTCGCTCTGCATACGACACTGCGTGGGTGGCGAGCTGGCGACCAT 473
 QY 389 TTCTCAAACTCACCAAAATCGCTTGTTCCTCAGTGTCTCAATTTGTTTAAATTAATAA 448
 Db 474 TTCTCTGATGATCTGAGAAGCCAGGTTTCTCAGGCCCTCAACTGGGTTTCAACAA 533
 QY 449 TCAGCTTAATGATGTTTCAATGGGGTCTGTTTAAATCACTCATATATCAATCAACCCGTT 508
 Db 534 CCAGCTCCAGGATGATCGTGGGTATCGAATCGCACTTTAGTTTATGCGATCGATGTCT 593
 QY 509 GCTTAAAGATCTCTATCTTCAACATTACCATGATGTTTGGCATTAATAAAGATGGAATGT 568
 Db 594 -----TAAACAGCAATCTGTTATCGCCCTCTCGGTTTGGAAAAC 635
 QY 569 TGGGGAAGATCAAAATAAAGGTCTAAGTTTATTTAGTCAAAATCTTGTCTTCAGCTAC 628
 Db 636 AGGCGACAGCAAGTACAAAGGTCTGAGTTTATTCAGAGAACTTAAGATTACTCAA 695
 QY 629 TGAATAAAGTCAACCATCTCCCATTTGTTTGAACATCATATTTCTTGGTTTGGTTGAGTA 688
 Db 696 TGAGGAAGATGATGTTGTCCTCC---GGATTTCAAAATAATCTTCTCTGCTCTGCTGCAAA 752
 QY 689 TCGGAAAACCTTGGACATATAACCTCTTTCAAAAAACAACAGATTTTGTGTTGATGCTACA 748
 Db 753 GGCATAAAGGTTGGGGATCATCTTCTTACGATCTTCCATTATCAAAATATTTGTGAC 812
 QY 749 TAAGAGGAATTTGGAGCAAAAGATGCCAT-----TCAAAATGAGATGGATGATPACTT 802
 Db 813 AACACGGGAAGCCAGGCTTACAGATGTTTCTCGGCAGCAGACAAATATTCAGCCAACAT 872
 QY 803 GCGGTATATCTCTGAAGGACTCGGTAAATTTATATGATTTGGAATATGTTGGAAGAAATATCA 862
 Db 873 GTTGAATCGTTTGAAGGTCTCGAGGAGTTATTTGACTGGAACAAGATTTATGAGGTTTCA 932
 QY 863 GATGAAAATGCTCTGTTTTCAACTCACCATCAGCAACAGCTGCTGCTTTCATTAATCA 922
 Db 933 AAGTAAAGATGATCTTCTCAGCTCCCTCCCTCCACTGCTGTGTACTGATGATATAC 992
 QY 923 TCAAAATCCTGTTGTCTTAAATTTTAAATTTTCACTTTTGGACAAGTTTGGTAATCAGT 982
 Db 993 AGGGGACGAAAATGTTTCACTTTTCTCAAACTCTGCTCGACAAATTCGGGGTGGCT 1052
 QY 983 CCCAACAGTTTATCTCATGATTTATTTATCCGACTTCTTATGTTGTTGACACAAATTTGAAG 1042
 Db 1053 GCCCTGTATGATTCATCGATCTGCTGGAACGCCCTTTCGCTGGTTGATTAACATGAGCA 1112
 QY 1043 ATTAGGAATTTCAACACCATTTCCAGAGTGGAATTTAAATAATTTTAGATGAAACATACAG 1102
 Db 1113 TCTCGAATCGGTGCGCATTTCAACAAGAAATCAAGAGAGCTCTTGATTTATGCTACAG 1172
 QY 1103 ATGTTGGGTGGAACGAG-----ATGAGCAAAATATTATCATGATGTTGTTAAC 1147
 Db 1173 ACATTTGGAGTGAAGGGGATCGTTGGGGCAGACAGACGCTTGTTCAGATCTCAACAC 1232
 QY 1148 ATGTCCTTTAGCTTTTGGTTTATTAAGGATCAATGGGTATGAAAGTTTCCCGAGATCCATT 1207
 Db 1233 CACAGCCCTCGGCTCGGAACTCTTCGCAATGACCGGATCAAAATGTTTCTTCAGACGTTT 1292
 QY 1208 GGCTGAAATTTACTAATGAATAGCTTTGAAAGACGAATATGAGCTC-----1254
 Db 1293 GAATTAATTTCAAGATGAAACCGGGGTTCTTCTCTCGGGCAAAACCATGTCGA 1352
 QY 1255 -TTGAAACATATCATGCGTCACATATATATATACCAAGA--GGATTATCTTCTGGAAAAC 1311
 Db 1353 ATTGAGAAGCGTGGTGAATCTTTTTCAGAGCTTTCGACCTTTCGATTTCTCCTGACGAAAGC 1412
 QY 1312 AAATCTTGAAGTCAGCTGATTTCTTCAAGAGATTAATATCCACTGATTTCAACAGCGTTT 1371
 Db 1413 TATGGACGATGCTAGAAAATTTGCAAGAACCAATATCTTAGAGAGGCACTTTGCAACGAAAT 1472
 QY 1372 CTAAATTAATTTCA-----CAAAAGAGGTGAAAATGCTTCTTAAGTTCCCTTATCAATAC 1423

Db 1473 CTCAACCAATAAAAACTATTCAAGAGATTGAGTACGTGTTGGAGTACCCTTGGCACAT 1532
Qy 1424 CGGTTTAGACGCTAAGCAACACTAGACGAAATATACAGCTTTACAACTGTAGACAAATACAAG 1483
Db 1533 GAGTATCCACGCTTAGAGCCAGAGTTATTTGATTATATGACGACAAATTTATGTATG 1592
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Qy 1544 TGTGAGAGATTCTACACCTGCCAATCTATTATTCGTGAAGAATTAAGAAGCTTTGAAAG 1603
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Qy 1604 GTGGGTGTAGAGAAATAAGTTGGACCCAGCTCAAGTCTTGTAGGCAAAAAGACCGCTACTG 1663
Db 1713 ATGTTGAAGGAATCCGGCATGGCAGATATANAATTTCACTCGACACCGAGTGGCGGAGGT 1772
Qy 1664 TTATTTCTGTGCTGCAACACTTTTCGTCTCCGAAATTTATCAGATCGCGTATTTTCATG 1723
Db 1773 TTATTTTTCATCAGCTACA-----TTTGAACCCGAAATTTCTGCCACTAGAATTCGCTT 1826
Qy 1724 GGCCAAAATGGCATATTAACATACAGTAGTTGATGACTTTTTTGATATCGGTGTTACAAT 1783
Db 1827 CACAAAATTTGGTTGTTTACAAGTCTTTTGTGATGATATGGCTGACATCTTTTGCAACAT 1886
Qy 1784 CGATGAATTCACCAACCTGATTCAATGTTGTAATAATGGAAATGAAATGATGTCGACAAAGGA 1843
Db 1887 AGATGAATTTGAAAAGTTTCACTGAGGAGTAAGAGATGGGATACATCTTTTGCTACATGA 1946
Qy 1844 TTGTTGTTACAGAGCAGTTTCGGATTTTATTTTATAGCAATTAAGAATGCAATCTGTTGGAT 1903
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Qy 1904 TGGAGATGAAGCTTTTAAATGGCAAGCGCGGATGTAACCTAGCCATGTTTATTCAACTTG 1963
Db 2004 AAATAATGATGTGTTAAGGTAAAGGATCAAGGACGTGACATGCTCGCTCACATAAGAAAAACCTG 2063
Qy 1964 GTTGGAACTAATGAATAGTATGTTGAGAGAAGCTATATATGACAAGAGATGCTTATGTGCC 2023
Db 2064 GGAGTTGTACTTCAATTTGTTATGTACAAGAAAGGAGTGGCTTGAAGCCGGTATATACC 2123
Qy 2024 AACATTAATGAATATATGAAACCGCTTACGTCTCATTTTGCAATTAGGCCCGGATTTGTCAA 2083
Db 2124 AACTTTGAAGAGTACTTAAGACTTATGCTATATCAGTAGGCCCTTGGACCGTGTACCCCT 2183
Qy 2084 GCCGGCTATTACTTTGTGGGGCCCAAAATTAACAGAGGATTTGTTGAAAAGCTCTGAATA 2143
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Qy 2144 TC---ATAATCTATTTAAGCTTAATGACACGAGGTCGACTTCTAAACGATATCCATAG 2200
Db 2244 TCCCTCAATATGTTTGAGCTTGTATCTCTTGTAGCTGGCGACTAACAAACGACCAACAAAC 2303
Qy 2201 CTTCAAGAGGGAATTTAAGGAAGGCAAAATTAACCGGTAGCATTTGCATTTGAGTAACGG 2260
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Search completed: February 16, 2006, 06:09:51
Job time : 501.49 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 08:16:57 ; Search time 249.08 Seconds
(without alignments)
2854.981 Million cell updates/sec

Title: US-10-041-018-22

Perfect score: 1720

Sequence: 1 MEAKIDELINNDPVWSSQNE.....DTATNLHDELLYIIDLHSL 335

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB_spool/US10041018/runat_14022006_080439_25149/app_query.fasta_1
-DB=Published Applications NA.New -QMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs04
-USER=US10041018 @CGN 1.1.380 @runat_14022006_080439_25149 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:
1: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:
2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
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13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	240	14.0	975	12	US-11-098-686-9415 Sequence 9415, Ap
2	240	14.0	1457619	12	US-11-098-686-8739 Sequence 8739, Ap
3	236	13.7	972	8	US-10-467-657-279 Sequence 279, App
4	236	13.7	972	8	US-10-467-657-4381 Sequence 4381, Ap

c	5	236	13.7	972	8	US-10-467-657-8261 Sequence 8261, Ap
	6	204	11.9	2987	12	US-11-194-246-99 Sequence 99, Appli
	7	189.5	11.0	948	12	US-11-119-351-5 Sequence 5, Appli
	8	174.5	10.1	960	8	US-10-793-626-1039 Sequence 1039, Ap
	9	174.5	10.1	2317	8	US-10-793-626-4357 Sequence 4357, Ap
	10	174.5	10.1	2987	8	US-10-793-626-3398 Sequence 3398, Ap
	11	164.5	9.6	903	12	US-11-098-686-9307 Sequence 9307, Ap
	12	164	9.5	888	12	US-11-194-246-139 Sequence 139, Ap
	13	164	9.5	2895	12	US-11-194-246-94 Sequence 94, Appli
	14	159	9.2	3444	8	US-10-793-626-4144 Sequence 4144, Ap
c	15	159	9.2	4045	8	US-10-793-626-3929 Sequence 3929, Ap
	16	155	9.0	966	12	US-11-092-140-11 Sequence 11, Appli
	17	152	8.8	1101	7	US-10-524-972-113 Sequence 113, Appli
	18	152	8.8	1101	8	US-10-524-647-125 Sequence 125, App
	19	150	8.7	1402	7	US-10-524-972-109 Sequence 109, App
	20	150	8.7	1402	8	US-10-524-647-121 Sequence 121, App
	21	147.5	8.6	1116	8	US-10-467-962B-40 Sequence 40, Appli
	22	145.5	8.5	783	8	US-10-793-626-223 Sequence 223, App
	23	145	8.4	5632	12	US-11-070-080-6 Sequence 6, Appli
	24	145	8.4	8814	12	US-11-070-080-41 Sequence 41, Appli
	25	144.5	8.4	561	12	US-11-092-140-10 Sequence 10, Appli
	26	139.5	8.1	888	12	US-11-129-143-184 Sequence 184, App
	27	138.5	8.1	888	8	US-10-967-671-1 Sequence 1, Appli
	28	138.5	8.1	888	8	US-10-967-671-3 Sequence 3, Appli
	29	135	7.8	1612	12	US-11-129-143-157 Sequence 157, App
c	30	134.5	7.8	2130	12	US-11-194-246-373 Sequence 373, App
c	31	134.5	7.8	2255	12	US-11-194-246-129 Sequence 129, App
	32	125.5	7.3	894	8	US-10-467-657-2849 Sequence 2849, Ap
	33	125.5	7.3	894	8	US-10-467-657-6749 Sequence 6749, Ap
	34	125	7.3	1155	7	US-10-524-972-111 Sequence 111, App
	35	125	7.3	1155	8	US-10-524-647-123 Sequence 123, App
	36	120.5	7.0	1087	12	US-11-092-140-15 Sequence 15, Appli
	37	112	6.5	950	12	US-11-070-080-35 Sequence 35, Appli
c	38	109.5	6.4	2872	8	US-10-240-708-91 Sequence 91, Appli
c	39	105.5	6.1	4434	12	US-11-140-930-16 Sequence 16, Appli
	40	103	6.0	3021	8	US-10-793-626-153 Sequence 153, App
	41	101	5.9	200	12	US-11-098-686-4594 Sequence 4594, Ap
c	42	101	5.9	1790	12	US-11-136-527-2252 Sequence 2252, Ap
c	43	97.5	5.7	1481	8	US-10-750-185-29175 Sequence 29175, A
c	44	97.5	5.7	1481	8	US-10-750-623-29175 Sequence 29175, A
	45	95.5	5.6	981	12	US-11-092-140-18 Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-11-098-686-9415
; Sequence 9415, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9415
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-9415

Alignment Scores:	2.47e-16	Length:	975
Pred. No.:	240.00	Matches:	90
Score:	44.6%	Conservative:	50
Percent Similarity:	28.7%	Mismatches:	125

Query Match:	14.0%	Indels:	49
DB:	12	Gaps:	8
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DB	82	TCATCTATTTCAGCCTGACCTGACATATCTCTCTCAAAAGGTAAAGATTACGTCCA	141
QY	41	AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal	60
DB	142	ATGCTTACTATCTCTCTCGACTTTTGGTTATTAATGAGGATGATATCTATCCATTA	201
QY	61	SerGlnIleValGlnLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn	80
DB	202	GCAATTTCAGTTGAGTTCTTCATGCAGCGACATCTACTCATGATGATGTATTAGATAAT	261
QY	81	AlaProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle	100
DB	262	GGCTATTAAAGAGTAATATCTATTACGCTCATACCTCTTTGGGACTGTTTCTACTATA	321
QY	101	AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGln	116
DB	322	CTTGCAGGTGACGCACCTGCTGCAAAAGCAATTTACTTTGTAGCAACCTATGATGTCAG	381
QY	117	-----LeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGlu	133
DB	382	AAATGTATCTTAACGATATCCCAAGCTCTTTACCAACACAGCA	423
QY	134	GluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuPro	153
DB	424	-----CATGGTGAATTCCTTGAGATATATAATCAAGG	456
QY	154	GluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGly-GlyLe	173
DB	457	GAATATGGAACAAACAAATATTATTAGAAATTTACTGGAAACACAGCTGGGTT	516
QY	173	uPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHisHisGlyHis	193
DB	517	ATTCAAGCAGCTTGTAAAGTGTGTCATGCAAGCAGGTGCTACTCCACACAGGTGGAT	576
QY	193	rLeuValProPheIleAsnLeu-LeuGlyIleIleTyrGlnIleArgAspTyrLeu	212
DB	577	GTGCTGCTTTATTGGCTATTAATCTTGTTATGCTTTTCAATCATAGATGATGATTA	636
QY	213	AsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGlu	230
DB	637	-----GACTTCTTACCTTCTAAAGATACAGGCAAACTGAAGGAGGAGATATACGA	687
QY	231	GluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln	250
DB	688	GAAGCAAAATTTACACCACTTTTATAC-----TATTTAAACAA	729
QY	251	ThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIle	270
DB	730	-----CTTTCTTTAGAGAAATAATAATA	753
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DB	754	TTTATAAAAAATTTCAAACTCATACTTTACAGATGAAGAGATACCTTACTATTACCAGG	813
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DB	814	GTCATCCATCAACAAATTTTGTATCAAAAAACACGGGAATTAGCCAATGTTATTTTCAA	873
QY	310	AspLeuAlaSerHisSerAspThrAlaThrAsnLeu	321
DB	874	AAAGCTTTAAACAAATTTAGAAATTTAACTAATGTT	909
RESULT 2			
US-11-098-686-8739			
; Sequence 8739, Application US/11098686			
; Publication No. US20060024696A1			

GENERAL INFORMATION:			
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.			
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES			
; FILE REFERENCE: 09531-128001			
; CURRENT APPLICATION NUMBER: US/11/098,686			
; CURRENT FILING DATE: 2005-04-04			
; PRIOR APPLICATION NUMBER: PCT/US03/31318			
; PRIOR FILING DATE: 2003-10-01			
; PRIOR APPLICATION NUMBER: US 60/416,395			
; PRIOR FILING DATE: 2002-10-04			
; NUMBER OF SEQ ID NOS: 11433			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8739			
; TYPE: DNA			
; ORGANISM: Lawsonia intracellularis			
US-11-098-686-8739			
Alignment Scores:			
Pred. No.:	3,08e-12	Length:	1457619
Score:	240.00	Matches:	90
Percent Similarity:	44.6%	Conservative:	50
Best Local Similarity:	28.7%	Mismatches:	125
Query Match:	14.0%	Indels:	49
DB:	12	Gaps:	8
US-10-041-018-22 (1-335) x US-11-098-686-8739 (1-1457619)			
QY	21	SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu	40
DB	630876	TCATCTATTTCAGCCTGACCTGACATATCTCTCTCAAAAGGTAAAGATTACGTCCA	630935
QY	41	AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal	60
DB	630936	ATGCTTACTATCTCTCTCGACTTTTGGTTATTAATGAGGATGATATCTATCCATTA	630995
QY	61	SerGlnIleValGlnLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn	80
DB	630996	GCAATTTCAGTTGAGTTCTTCATGCAGCATTTACTACATGATGATGTATTAGATAAT	631055
QY	81	AlaProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle	100
DB	631056	GGCTATTAAAGAGTAATATCTATTACGCTCATACCTCTTTGGGACTGTTTCTACTATA	631115
QY	101	AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGln	116
DB	631116	CTTGCAGGTGACGCACCTGCTGCAAAAGCAATTTACTTTGTAGCAACCTATGATGTCAG	631175
QY	117	-----LeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGlu	133
DB	631176	AAATGTATCTTAACGATATCCCAAGCTCTTTACCAACACAGCA	631217
QY	134	GluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuPro	153
DB	631218	-----CATGGTGAATTCCTTGAGATATATAATCAAGG	631250
QY	154	GluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGly-GlyLe	173
DB	631251	GAATATGGAACAAACAAATATTATTAGAAATTTACTGGAAACACAGCTGGGTT	631310
QY	173	uPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHisHisGlyHis	193
DB	631311	ATTCAAGCAGCTTGTAAAGTGTGTCACCTGAAAGCAGGTGCTACTCCACACAGGTGGAT	631370
QY	193	rLeuValProPheIleAsnLeu-LeuGlyIleIleTyrGlnIleArgAspTyrLeu	212
DB	631371	GTGCTGCTTTATTGGCTATTAATCTTGTTATGCTTTTCAATCATAGATGATGATTA	631430
QY	213	AsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGlu	230
DB	631431	-----GACTTCTTACCTTCTAAAGATACAGCAAACTGAAGGAGGAGATATACGA	631481

```
QY 231 GluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln 250
Db 631482 GAAGGCAAAATTACACCACTTTTATAC-----TATTTAAACA----- 631523
QY 251 ThrGluGlnHisAsnGluLeuLeuArgIleLeuLeuLeuArgThrSerAspLysAspIle 270
Db 631524 -----CTTTCTTTAGAGAAATAATAATA 631547
QY 271 LysLeuLysLeuIleGlnIleLeuGluPhe---AspThrAsnSerLeuAlaTyrThrLys 289
Db 631548 TTTATAAAAAAATTTCAACTCATATTTACAGATGAAGATACCTATTATACAGG 631607
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
Db 631608 GTCATCCATCAACAAATTTTGATCAAAAAACACGGGAATTAGCAATGTTTATTTCAA 631667
QY 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeu 321
Db 631668 AAAGCTTTTAAACAATTTAGAAATTATTAACTAATGTT 631703

RESULT 3
US-10-467-657-279
; Sequence 279, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 279
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-279

Alignment Scores:
Pred. No.: 6.8e-16 Length: 972
Score: 236.00 Matches: 66
Percent Similarity: 48.8% Conservative: 61
Best Local Similarity: 25.4% Mismatches: 109
Query Match: 13.7% Indels: 24
DB: 8 Gaps: 6

US-10-041-018-22 (1-335) x US-10-467-657-279 (1-972)
QY 3 AlalysileAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu---Ser 21
Db 49 GCCAAGTCAATGAAGTCATCAACCGT-----CGGTGCAATCCGATCGCA 96
QY 22 LeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
Db 97 CTGATTTGCAAAATCGGTACATATATCATCAGCGCGGCGCAAAACGCTCGGTCCGATT 156
QY 42 LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
Db 157 ATGACGATTTTGGCGGTAAGCGGTGCTGTTATGATGACGAAACTGTATTCCGTGGCA 216
QY 62 GlnIleValGluLeuLeuIleAsnSerSerLeuIleAspIleGluAspAsnAla 81
Db 217 GCGATGTCAGTATTTACCACTTCACACTCTGCACGACGATGTCGATGAAGC 276
QY 82 ProLeuArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
Db 277 GATTTGCGCGTGGCGGCAACGGCAACAATCTGTTGGCAATGCGGCGGCGATGTTG 336
```

```
QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal-----SerGlnLeuThr 118
Db 337 GTTGGCGACTTTTATATATACCGTGCATTTCACTGATGTTGCTCGGCAGTATCGGC 396
QY 119 ThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeu 138
Db 397 GTTTTGAAGTGTATGCGGATGCGACCAACATCATTTGCCCGGAGGAGGTCATCGAGTG 456
QY 139 HisArgGlyGlnGlnLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThr 158
Db 457 ATGAACATCGGCAATACGGACATT-----ACC 483
QY 159 GlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeu 178
Db 484 GAAGAACATATATCCGATCATCCATATAAACGGCAAAATTTTGAAGTCGCGCT 543
QY 179 ArgLeuMetGluAlaLeuSerProSerSer---HisHisGlyHisSerLeuValProPhe 197
Db 544 CAAATCGGCGCAATTTTGGGCAAAAGCTTCCCGGGCAGCAACAGGCTTTGAAAGACTAC 603
QY 198 IleAsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPhe 217
Db 604 GGTATGTACGTGCGGTACGGCATTTCCAGATTATTGACGATGCTGTGATTATTCGGGGAA 663
QY 218 GlnMetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPhePro 237
Db 664 ACCGAGAACAACAGTAAACAGTCGGGCGAGATTGCGGGAAGGAAACCGACCTCGCT 723
QY 238 IleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIle 257
Db 724 TTGATTTATCTGATGCGT-----CAGGGTTCCGAAACAGGTTGCGAAGCATGTG 771

RESULT 4
US-10-467-657-4381
; Sequence 4381, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4381
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4381

Alignment Scores:
Pred. No.: 6.8e-16 Length: 972
Score: 236.00 Matches: 66
Percent Similarity: 48.8% Conservative: 61
Best Local Similarity: 25.4% Mismatches: 109
Query Match: 13.7% Indels: 24
DB: 8 Gaps: 6

US-10-041-018-22 (1-335) x US-10-467-657-4381 (1-972)
QY 3 AlalysileAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu---Ser 21
Db 49 GCCAAGTCAATGAAGTCATCAACCGT-----CGGTGCAATCCGATCGCA 96
QY 22 LeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
Db 277 GATTTGCGCGTGGCGGCAACGGCAACAATCTGTTGGCAATGCGGCGGCGATGTTG 336
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[illegible]

RESULT 5

US-10-467-657-8261/c

US-10-407-037-02017C
; Sequence 8261, Application US/10467657

; Publication No. US20050260581A1

: GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-0

; PRIOR APPLICATION NUMBER: GB-0103424.8

;
; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

```
; SOFTWARE: SeqWin99, version 1.04
```

; SEQ ID NO 826

; LENGTH: 972

TYPE: DNA

ORGANISM: *Neisseria gonorrhoeae*

US-10-467-657-8261

Alignment Scores:

Pred. No.: 6.8e-16

Percent Similarity:	48.8%	Conservative:	61
Best Local Similarity:	25.4%	Mismatches:	109
Query Match:	13.7%	Indels:	24
DB:	8	Gaps:	6

US-10-041-018-22 (1-335) x US-10-467-657-8261 (1-972)

	Qy	3	AlaLysIleAspGluLeuIleAsnHisSerValTrpSerSerGlnAsnGlu---Ser	21
	Dd	924	GCCAAAGTCAATGAAGTCATCAACCGT-----GGGTGCAAATCCGATGTGC	87
	Qy	22	LeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn	41
	Dd	876	CTGATTTCCAAATCGGTACATATATCATCAGCGCGCGCAACCGCTCGTCCGATT	81
	Qy	42	LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer	61
	Dd	816	ATGACGATTTCGGCGGTAAAGCGTGCTGTTATGATGACGAGAAACTGTATTGCTGC	75
	Qy	62	GlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsnAla	81
	Dd	756	GCAGTGGTGCAGTTTATCCACACTTCCACACTCTCTGCCACGACGATGTCGTGCATGAAGA	69
	Qy	82	ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn	10
	Dd	696	GATTTCGGCGGTGGCGGCAACGCAACAACATCTGTTCCGCAATGCGCGCGCAGTGTG	63
	Qy	102	ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal-----SerGlnLeuThr	11
	Dd	636	GTTGGCGACTTTTATATACCCTGTCATTCAACTGATGTTGCTCGGCAGATATGCG	57
	Qy	119	ThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeu	13
	Dd	576	GTTTTGGAAGTAGTCGGGATGCCACCAACATCATTCGCCAGGAGGAGGTTCATGACGTG	51
	Qy	139	HisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThr	15
	Dd	516	ATGAACATCGGCNAATACGGACATT-----ACC	49
	Qy	159	GlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeu	17
	Dd	489	GAAGAACATAATATCCGAGTCATCCAATAAACCAGCGCAAAATTTGTTGAAGCTGCCGT	43
	Qy	179	ArgLeuMetGluAlaLeuSerProSerSer--HisHisGlyHisSerLeuValProPhe	19
	Dd	429	CAAGTCGGCGCAATTTTGGCGAAAGCTTCCC CGCGCACGACCAACAGGCGCTTGAAAGACTAC	37
	Qy	198	IleAsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPhe	21
	Dd	369	GGTATGTACGTGGTACGGCATTCAGATTAATTGACGATGTGCTGGATATTTCGGGGAA	31
	Qy	218	GlnMetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPro	23
	Dd	309	ACCGAAGAACAGGTAAAAAGTCGGCGACGATTTGGCGGAAGGAAAACCGACCCCTGCCT	25
	Qy	238	IleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIle	25
	Dd	249	TTCGATTATCTGATCGGT-----CAGGTTCCGAACAGGTTGCGAACAGTGTG	20

RESULT 6

US-11-194-246-99

00-11-194240-25
; Sequence 99, Application US/11194246

Publication No. US20050272089A1

GENERAL INFORMATION:

APPLICANT: Mott, John

APPLICANT: Trepod, Catherine

APPLICANT: Arvidson, Staffan

; TITLE OF INVENTION: CRIT

INVENTION:	USE:
TITLE OF INVENTION:	USE:
TITLE OF INVENTION:	USE:

FILE REFERENCE: 00592.US1 (M&R 268.059201

; CURRENT APPLICATION NUMBER: US/11

; CURRENT FILING DATE: 2005-08-01

QY 145 AspIleTyrTrpArgAspPheLeuProGluIlelleProThrGlnGluMetTyrLeuAen 164
 Db 418 CAGATGGTGGTGCAGAAC-----GACCTTACGACCGCTGTAGACGCTATCTTGAA 468
 QY 165 MetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeu-----MetGlu 182
 Db 469 GTCATTACCGGACAGACGCTGGCTGTTGGCGCTGCTGGCGCTGCTGGCGCTGCTGG 528
 QY 183 AlaLeuSerProSerSerHisGlyHisSerLeuValProPheIleAsnLeuGly 202
 Db 529 GCGGACGCTCCGAGCAGCAGAGAG---GAAGCTCTGGAGCGGTTTGGCACCACCAATCTGGGT 585
 QY 203 IleIleTyrGlnIleArgAspPheTyrLeuAsnLeuLysAspPheGlnMetSerSerGlu 222
 Db 586 ATGGCGTTCAGCTTGTGATGATGCTGCTGATGATGATGATGATGATGATGATGATGATG 645
 QY 223 LysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleVal----- 239
 Db 646 AAGACCGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 705
 QY 239 ----- 239
 Db 706 GAGGCTGGCTCGCGGAGATCGTATTTCTGGAGCGGCTCATTCGAGAGAGGAGGAGCAG 765
 QY 240 -----HisAlaLeuAsnPheThrLysThrLysGly----- 249
 Db 766 ACTGAGGACGATCTGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 825
 QY 250 -----GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeu 262
 Db 826 AGATCGCGCGCGGAGTCTATGCGGACGAGCTGTTGAGCCCTGTCATTTTC----- 882
 QY 263 LeuArgThrSerAspLysAspLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLys 282
 Db 883 -----CCGATAGCAGACGCTGCGCGCTCTGATCGAACGCTTCAGITTCACGGTG 933
 QY 283 Asn 283
 Db 934 AAT 936

RESULT 8
 US-10-793-626-1039
 ; Sequence 1039, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: P3480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1039
 ; LENGTH: 960
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: nucleic acid sequence
 US-10-793-626-1039

Alignment Scores:
 Pred. No.: 3,98e-09 Length: 960
 Score: 174.50 Matches: 74
 Percent Similarity: 42.9% Conservative: 70
 Best Local Similarity: 22.0% Mismatches: 131
 Query Match: 10.1% Indels: 61
 DB: 8 Gaps: 13

US-10-041-018-22 (1-335) x US-10-793-626-1039 (1-960)

QY 3 AlaIleLysAspGluLeuIleAsnAsp-----ProValTrpSerSerGlnAsnGlu 20
 Db 4 GCAAGATTAAAC-----ATTAAACACGAAATAAAGAAAGTAGAAAGCGACTTGAAGAA 57
 QY 21 SerLeuIleSerLysProTyrAsn-----HisIleLeuLeuLysPro 34
 Db 58 GCAATTATAAGTTCGATCAAAACATTACAGAAGCGCTCATTCATTTACTATCTTTCAGGG 117
 QY 35 GlyLysAsnPheArgLeuAsnLeuLeuValGlnIleAsnArgVal-----MetAsnLeu 52
 Db 118 GGAAGAGAGTGTAGACCGCTTTTGTATTATTAAAGTGGTCAATTTGGCTCTAACACAAA 177
 QY 53 ProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsnSerSerLeu 72
 Db 178 CCTCAGAAGACACGATGCTGTCAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGT 237
 QY 73 LeuIleAspAspIleGluAsnAlaProLeuArgGlyGlnThrThrSerHisLeu 92
 Db 238 GTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 297
 QY 93 IlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGln 112
 Db 298 AAATGGGACCAAGTACAGCTATTTTAAACAGGAAATTTCTTACTTGTCTATGGGCTCAAG 357
 QY 113 LeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIlePheAsn 132
 Db 358 CATTTATCTGAATCAGT-----GATACCTGTCCTCATTCGACCAT-----TCT 402
 QY 133 GluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeu 152
 Db 403 AAATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
 QY 153 ProGluIleIleProThrGlnGluMet-----TyrLeuAsnMetValMetAsnLysThr 170
 Db 448 GATCAATTTAATAGCAATCAAACTTACTTAATTTACTTACGTCGTATCAACCGTAAACA 507
 QY 171 GlyGlyPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerHisHis 190
 Db 508 GCACTTCTTAACTGTCTACAAAGTGTGGATGATTTCCAAATCGCTCAAAATGAC 567
 QY 191 -----GlyHisSerLeuValProPheIleAsnLeuGly 202
 Db 568 GTTATTCGTAAATTAATAATGATCGCAT-----TATATAGGT 606
 QY 203 IleIleTyrGlnIleArgAspPheTyrLeuAsnLeuLysAspPheGlnMetSerSerGlu 222
 Db 607 ATGAGTTTCCAAATAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 QY 223 LysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHisAlaLeu 242
 Db 667 AAGCCGGTGGTGTAGTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
 QY 243 AsnPheThrLysThr-----LysGlyGlnThrGluGlnHis 254
 Db 727 CGAAAAAATAAGACTTTTAAAGATAAAATTTCAACATTAATCTCAGAGTCTCAACAT 786
 QY 255 AsnGluIleLeuArgIleLeuLeuArgThrSerAspLysAspLysLeuLysLeu 274
 Db 787 GCCTTTGAAACTTGTATATAAATAATAGACAGTCCGAAAGCATAGAACAAATCAAAACAA 846
 QY 275 IleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGln 294
 Db 847 ATA-----AGTGAAAGTATTATAATAA 870
 QY 295 LeuValAsnMetIleLys-----AsnAspAsnGluAsnLysTyrLeu 308
 Db 871 GCAATCAATTTAATCGATGAATTAGAGGATGGTCTTAATAAAGAACTA 918

RESULT 9
 US-10-793-626-4357
 ; Sequence 4357, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:


```

Db      1488  ATGAGTTTCCAAATAATAGATGATGCTGAGATTTTACTAGTCTCGAAAGAACAACCTGGT 1547
Qy      223  LysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHisAlaLeu 242
Db      1548  AAGCCGGTTGGTAGTGACCTTATGAATGGTCATATTACATTACCTGCTACTATTAGAAATG 1607
Qy      243  AsnPheThrIysThr-----LysGlyGlnThrGluGlnHis 254
Db      1608  CGAAAAAATAAGACTTTTAAAGATAAAATTTCAACACTTAATCCTGACAGTCTCAACAT 1667
Qy      255  AsnGluIleLeuArgIleLeuLeuLeuAqThrSerAspLysAspIleLysLeuLeu 274
Db      1668  GCCTTTGAAACTTGTATACAAATAATTAGACAGTCGNAAGAGCATAGAACAACTCAAAACAA 1727
Qy      275  IleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGln 294
Db      1728  ATA-----AGTGAAGAAGTATTATTAAATATAA 1751
Qy      295  LeuValAsnMetIleLys-----AsnAspAsnGluAsnLysTyrLeu 308
Db      1752  GCAATCAATTTATTCGATGAATTAGAGGATGGTCTCTAATAAGAACTA 1799

RESULT 10
US-10-793-626-3398
; Sequence 3398, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3398
; LENGTH: 2987
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3398

Alignment Scores:
Pred. No.: 1,72e-08 Length: 2987
Score: 174.50 Matches: 74
Percent Similarity: 42.9% Conservative: 70
Best Local Similarity: 22.0% Mismatches: 131
Query Match: 10.1% Indels: 61
DB: 8 Gaps: 13

US-10-041-018-22 (1-335) x US-10-793-626-3398 (1-2987)

Qy      3  AlaIysIleAspGluLeuIleValSerGlnAsnAsp-----ProValTyrSerSerGlnAsnGlu 20
Db      885  GCAAGTTAAAC-----ATTAAACAAGAAATAAGAAAGTAGAAGGACGCTTGAGAA 938
Qy      21  SerLeuIleSerLysProTyrAsn-----HisIleLeuLysPro 34
Db      939  GCAATTATAAGTTCTGATCAACATTACAAGAGCCTCATTTCTATTCTTCTCAGG 998
Qy      35  GlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgVal-----MetAsnLeu 52
Db      999  GGAAAAAGAGTTAGACCCCGCTTTTGTATTATTTAAAGTGGTCAATTTGGCTCTTAACAACAAA 1058
Qy      53  ProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuHisAsnSerSerLeu 72
Db      1059  CCTTCGAGACACGATGTCGTGACGAGTAGCTTTTAGAACTAATTACATGGCTACCTTTA 1118
Qy      73  LeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeu 92

```



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; Sequence 139, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139
; LENGTH: 888
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: ispa gene sequence
US-11-194-246-139

Alignment Scores:
Pred. No.: 5.17e-08 Length: 888
Score: 164.00 Matches: 63
Percent Similarity: 44.2% Conservative: 51
Best Local Similarity: 24.4% Mismatches: 124
Query Match: 9.5% Indels: 20
DB: 12 Gaps: 7

US-10-041-018-22 (1-335) x US-11-194-246-139 (1-888)
Qy 1 MetGluAlaLysLeuAspGluLeuLeuAsnAspProValTrpSerSerGlnAsnGlu 20
Db 55 TTAGAAGCTCAATTGAAGGCATT-----GAAAGTCATAATGCG 93
Qy 21 SerLeuLeuSerLysProTyrAsnHisLeuLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 94 CTTTGGCTT---GAGGCGATGAATAACGCATTATTCTTGGCGGTAAAGCGAGTTGCGCCT 150
Qy 41 AsnLeuLeuValGlnLeuAsnArgValMetAsnLeuProLysAspGlnLeuAlaLeuVal 60
Db 151 TTCTTAGTTACGACAGCTCAATGCTTGGCGCAGAGAAACAACTTAGATTACGCT 210
Qy 61 SerGlnLeuValGlnLeuLeuHisAsnSerSerLeuLeuLeuAspAspLeuGlu-----78
Db 211 GCTGCTGCCATTGAAGCCATTACGCTTATTCCTTAATTCACGATGATTACCTGCAATG 270
Qy 79 AspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSer 98
Db 271 GATGATGACAAATTACGCGCGTGACATCCTACTTGTCTATTCATATCAATTTGATGAAGCTACA 330
Qy 99 ThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGln-----116
Db 331 GCTATTTCTGGGCGATGACATGCAAGTTTGCATTGGAATTAATTAACCAACACCG 390
Qy 117 ---LeuThrThrLysGluProLeuTyrHisAsnLeuLeuThrIlePheAsnGluGluLeu 135
Db 391 AATATTCTACTGAACAAAACCTGGCTTAAATTCAAATTTAGCGCAAGCGTGGTG 450
Qy 136 IleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluLeu 155
Db 451 CAAGGAATGTGTGTAGGCGCAAGTTAGATCTATTCTGAGCAT-----AAACAG 501
Qy 156 IleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArg 175
Db 502 ATTAGTTAAGTGAATTAGAATTA---ATTCACTCGTAACAAAACGGGTGCAATGCTAAT 558
Qy 176 LeuThrLeuArgLeuMetGluAlaLeuLeuSerPro-----SerSerHisGlyHis 192
Db 176 LeuThrLeuArgLeuMetGluAlaLeuLeuSerPro-----SerSerHisGlyHis 192

```

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Db 559 GCGCATTTGAAATAGGTTTCAATTTCTCCGCAATTTTACCGACAAAGGTTAGAACAA 618
Qy 193 SerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleAspAspTyrLeu 212
Db 619 TCCTTAACACAATATGCGAAGCCATTGGTTTAGCCTTTCAAGTTCAAGACGATATTTTA 678
Qy 213 AsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThrGluGly 232
Db 679 GATATTGAAGCGCATAGTAGTCAGAAATTTGGCAACAGTGGTCCGATCTTGATTAGAT 738
Qy 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln 250
Db 739 AAAAGTACATATCCAAATTAATTCTTGATTAAGTGGTGCACAAAACAAAAGGCCAA 792

RESULT 13
US-11-194-246-94
; Sequence 94, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Sequence of the ispa coding sequence and flanking regions.
US-11-194-246-94

Alignment Scores:
Pred. No.: 2.36e-07 Length: 2885
Score: 164.00 Matches: 63
Percent Similarity: 44.2% Conservative: 51
Best Local Similarity: 24.4% Mismatches: 124
Query Match: 9.5% Indels: 20
DB: 12 Gaps: 7

US-10-041-018-22 (1-335) x US-11-194-246-94 (1-2885)
Qy 1 MetGluAlaLysLeuAspGluLeuLeuAsnAspProValTrpSerSerGlnAsnGlu 20
Db 1055 TTAGAAGCTCAATTGAAGGCATT-----GAAAGTCATAATGCG 1093
Qy 21 SerLeuLeuSerLysProTyrAsnHisLeuLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 1094 CTTTGGCTT---GAGGCGATGAATAACGCATTATTCTTGGCGGTAAAGCGAGTTGCGCCT 1150
Qy 41 AsnLeuLeuValGlnLeuAsnArgValMetAsnLeuProLysAspGlnLeuAlaLeuVal 60
Db 1151 TTCTTAGTTACGACAGCTCAATGCTTGGCGCAGAGAAACAACTTAGATTACGCT 1210
Qy 61 SerGlnLeuValGlnLeuLeuHisAsnSerSerLeuLeuLeuAspAspLeuGlu-----78
Db 1211 GCTGCTGCCATTGAAGCCATTACGCTTATTCCTTAATTCACGATGATTACCTGCAATG 1270
Qy 79 AspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSer 98
Db 1271 GATGATGACAAATTACGCGCGTGACATCCTACTTGTCTATTCATATCAATTTGATGAAGCTACA 1330
Qy 99 ThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGln-----116
Db 99 ThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGln-----116

```


Qy	256	GluIleuArgIleLeuLeuLeuAspThrSerAspLysAspIleLysLeuIle	275
Db	1527	TATCTTGCTATGAACGCTTAATAACAATTCTGTAT-----	1492
Qy	276	GlnIleLeuGluPheAspThrAsnSerLeuAla---TyrThrLysAsnPheIleAsn-Gl	294
Db	1491	-----CAATATGATACTTCGTAAATTAAGTGATATGTAGATTTAATCTATAACAGA	1441
Qy	294	nLeuValAsnMetIleLysAsn	301
Db	1440	GACCATTAAATTTATAAAAAAT	1419

Search completed: February 16, 2006, 11:08:15
Job time : 521.08 secs

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	Query Match	2.9%;	Score 46.2;	DB 12;	Length 96988;
	Best Local Similarity	46.8%;	Pred. No.12;		
	Matches 180;	Conservative 0;	Mismatches 203;	Indels 2;	Gaps 1;
Qy	1106	ATATAAAAC	CTAAAGCTGATTCAAATAC	TGGAATTCGACACCAAAATTCATTGGCGCTACACCA	1165
Db	61010	AAATTGCAATCAAAAACCTTTTAAATAGTGAAAATATATACCTACATTCGAAAAA	AAAAA		61069
Qy	1166	AAAAATTTTATTAATCAATTAGTAGTAATGATAAAAAATGATAATGAAAATAAGTATTTTAC	1225		
Db	61070	CAAAATATAATACTACAAACCTAAATTTTAAATGAAAAATCTCTCTAAATGGTGAAAAATAT	61139		
Qy	1226	CTGATTTGGCTTCGCAATTCGCACACCGCCACCAATTTACATGACGAATTTGTTTATATATAA	1285		
Db	61130	ATACCCCTAAATTGGAAATATAGGAACCCCAATTAATATCTATATACTAATATTTAAATGNA	61189		
Qy	1286	TAGACCCTTATCCGAATTTGTGAAATAAATTTGATCAATCAAAATTTAGTGGAGGAAGATAGT	1345		
Db	61190	TCAAAATTTTCTTTTAAATAGTTTGAATAATATATGCGCTTAAATTCGAAATAGAGAACCCCAAT	61249		

```
QY 1346 CAGAAATAAGCCTTCTCTCCTC--CTCTTTCGCATCTATACATACGATTTTCATATATAC 1403
Db 61250 ATAACAATTTAAATTTATTTCTCATTTCTTTTGGTTGAATAGATTTAAATATAAAATTTGTG 61309
QY 1404 GTTTCATGCATCATCTTTTGTATATATCTCAAAAGATCTCTTAGTTCGCAAAATAGTCAA 1463
Db 61310 GTTTTATTTGTCACCTTTTAAATTTTCNAATATATTATTTGAGTGTCTATTTATGTCTA 61369
QY 1464 ATCTTCAAAATTTATAGCCTTTATAT 1488
Db 61370 AAAAACTTTGTAATGCTATTTTGT 61394
```

RESULT 2

```
US-09-925-065A-748963/c
; Sequence 748963, Application US/09925065A
; Publication No. US20040181048A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single
```

```
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925,065A
```

```
; CURRENT FILING DATE: 2001-08-08
```

```
; PRIOR APPLICATION NUMBER: US 60/243,096
```

```
; PRIOR FILING DATE: 2000-10-24
```

```
; PRIOR APPLICATION NUMBER: US 60/252,147
```

```
; PRIOR FILING DATE: 2000-11-20
```

```
; PRIOR APPLICATION NUMBER: US 60/250,092
```

```
; PRIOR FILING DATE: 2000-11-30
```

```
; PRIOR APPLICATION NUMBER: US 60/261,766
```

```
; PRIOR FILING DATE: 2001-01-16
```

```
; PRIOR APPLICATION NUMBER: US 60/289,846
```

```
; PRIOR FILING DATE: 2001-05-09
```

```
; NUMBER OF SEQ ID NOS: 957086
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 748963
```

```
; LENGTH: 645
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
US-09-925-065A-748963
```

```
Query Match 2.8%; Score 44.6; DB 6; Length 645;
Best Local Similarity 47.6%; Pred. No. 5;
Matches 131; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
```

```
QY 181 GACGTTTTTTTGAAGCAAAAGCTCAAGACAGATGTGTACAAAACCATGTAAGGC 240
Db 550 GAACATTTTTCACAAAACATATCTTTATAAACTAACTCCAGATAGTTAATAAAGC 491
QY 241 TCATTTTCAAGAAGCTACTAATAGAAAGAGACAAAGAGTTTACGAGTCTCGAAATCA 300
Db 490 TGATAGATATTAAATGTAAAAAGAACATGAATAAGCAACTAGAAATATTAGAAAAACA 431
QY 301 ATGGAGGCCAAGATAGATGAGTGCATATATGATCCTGTGTGTCAGCCAAATGAA 360
Db 430 ATAGAAAAATAAGTACTAGGTTCACATAAACTGATCCTATATAAAGTCACCCAAATGT 371
QY 361 AGCTTGATTTCAAAACCTTATATATCATATCTTTTGAACCTGGCAAGAACTTTAGACTA 420
Db 370 GGGCTCTGGGTATATAATAATAATAATAATAATAATAATAATAATAATAATAAGTA 311
QY 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTT 455
Db 310 AATACATCTTCTTAATTTATATCTTAAGAAATTT 276
```

RESULT 3

```
US-10-240-708-25/c
```

```
; Sequence 25, Application US/10240708
```

```
; Publication No. US20050282157A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: OLEK, Alexander
```

```
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 25
; LENGTH: 6583
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-25
```

```
Query Match 2.8%; Score 44.4; DB 8; Length 6583;
Best Local Similarity 51.0%; Pred. No. 12;
Matches 105; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 1022 CCCTTAACCTTCACTAAACGAAAGGTCAAACTGAGCAACACACAAATCTTAAGAATTC 1081
Db 5235 CCTCAAAACCAAAATTTCAAAAAACAATCTCTTACCTCTCAAAATATATATCTAAAAAAT 5176
QY 1082 TCCTGTGTAGGACAAGTGATAAAGATATAAAACTAAAGCTGATTCAAATACTGGAATTCG 1141
Db 5175 TTTCTCTCACTCCGAAAAAAGCAATATATATATATATATATATATATATATATATATAT 5116
QY 1142 ACACCAATTCATTTGGCCTACACCAAAAAATTTTATTAATCAATAGTGAATATGATAAAA 1201
Db 5115 AAACCAAAACAAATATCTCGAATAATATTTCTTTTAAACGTAATAAAAAATAACTAAAT 5056
QY 1202 ATGATAATGAAATAAGTATTTTACCT 1227
Db 5055 ACGATAATAAAAAATAACTATATACAT 5030
```

RESULT 4

```
US-09-925-065A-748964/c
; Sequence 748964, Application US/09925065A
; Publication No. US20040181048A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single
```

```
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925,065A
```

```
; CURRENT FILING DATE: 2001-08-08
```

```
; PRIOR APPLICATION NUMBER: US 60/243,096
```

```
; PRIOR FILING DATE: 2000-10-24
```

```
; PRIOR APPLICATION NUMBER: US 60/252,147
```

```
; PRIOR FILING DATE: 2000-11-20
```

```
; PRIOR APPLICATION NUMBER: US 60/250,092
```

```
; PRIOR FILING DATE: 2000-11-30
```

```
; PRIOR APPLICATION NUMBER: US 60/261,766
```

```
; PRIOR FILING DATE: 2001-01-16
```

```
; PRIOR APPLICATION NUMBER: US 60/289,846
```

```
; PRIOR FILING DATE: 2001-05-09
```

```
; NUMBER OF SEQ ID NOS: 957086
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 748964
```

```
; LENGTH: 645
```

```
; TYPE: DNA
```



```

; ORGANISM: Homo sapiens
US-09-925-065A-748964

Query Match      2.8%; Score 44.2; DB 6; Length 645;
Best Local Similarity 47.3%; Pred. No. 6.1;
Matches 130; Conservative 1; Mismatches 144; Indels 0; Gaps 0;

Qy 181 GACCTTTTGAAGCAAAAGGCTCAAGACAGATGCTTACAAACCATGTAAGGC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 550 GAACATTTTACAAAACATATCTTTATAAACTAACTCCAGAAATAGTTAATAAGC 491
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 TCATTTTCAAGAGCTACTAATAGAAAGAGAAACAAAGAGTTTACGAGTCTGGAATCA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 490 TGATAGAATATTAAATGTAAGAAAGACATGAATAAGCAACTAGAAATATTAGAAACA 431
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 ATGGAGCCCAAGATAGATGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 430 ATAGAAATAAAGTAACTGAGTTCACTAAAGCTGATCTATATAAGTCAACCAATGCT 371
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 AGCTTGATTTCAAAACCTTATAATCACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 370 GGCTCTGGGTATATATTAATAATAATTAATTAATTAATTAATAATAATAAGTA 311
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 421 AATTTAATAGTTCAAAATTAACAGAGTTTATGAATTT 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 310 AATACATCTCTTCTTAATTTATACCTAAAGAAATTT 276
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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RESULT 5
US-09-925-065A-292262
; Sequence 292262, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292262
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-292262

Query Match      2.8%; Score 43.8; DB 6; Length 623;
Best Local Similarity 54.0%; Pred. No. 7.4;
Matches 87; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

Qy 1070 TTCTAGAATTCCTCTGAGGCAAGTATGAAGATATAAAGCTAAAGCTGATTCAAA 1129
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 263 TTCTCCGATTTGTTATGGTTGCGAATTCACAAAATATATCCCTCTAAAGACTCATCGAA 322
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1130 TACTGGAATTCGACCAACCAATTCATGGCCCTACACAAAATTTTATTAATCAATTAAGTA 1189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 323 TATGGCAATTTACTGCACTTAATTAATGATCGATTAATAATTTATCTTTAAATAATGA 382
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1190 ATATGATAAAAATGATAATGAATAAGAAATGATTTTACCTGAT 1230
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 383 ACAAGCCAGGATAAAACCAAGATAAATAGTAGTACTTACCTCAT 423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 6
US-09-925-065A-203862/c
; Sequence 203862, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203862
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-203862

Query Match      2.7%; Score 42.6; DB 6; Length 602;
Best Local Similarity 48.9%; Pred. No. 13;
Matches 114; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 1260 TTTCATGACGAATGTTATATATATATATAGACCACTTATCCGAATGTGAATAAATGAT 1319
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 588 TTAATACTACAATGCTGTGATTTTGAACCTCTGTAAATGCAATGATTTTAAATGCT 529
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1320 CAATCAAAATAGTGGAGGAGATAGTCAGAAATAAGCCCTTCTCTCTCTCTCTCCAT 1379
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 528 CTTTTCAAATGCTGTGCTAGTATACAGAAAACAGTTGACCTTTTGTATTTTGACCTC 469
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1380 CTATACATACGATTTTCATATATATATATATGATCATCTTTTGTATATATCTCAAAAAG 1439
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 468 ATATCTTACCTGCTGCTAAATTTATTTATTTAGTTCTAGAACTTTCTTAGATCTTTTG 409
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1440 ATCTCTAGTTCGCAAAATAGTCAAAATCTTCAAAATTTATAGCCTTTATATTTT 1492
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 408 ATTTTTCACACTGATAATTTAATTTGCAAAATAAATATATCAGTTTATTTTCT 356
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 7
US-09-925-065A-913429
; Sequence 913429, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 913429
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-913429

Query Match      2.7%; Score 42.6; DB 6; Length 658;
Best Local Similarity 48.9%; Pred. No. 14;
Matches 114; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 1260 TTACATGACGAATGTTATATATATATAGACACATTTATCCGAATTCGAAATTAATATGAT 1319
Db 28 TTAATACTACTCAATGCTTGAATTTTGAACCTTGTAAATGGCAATGATTTTAAATGCT 87

QY 1320 CAATCAAAATTAGTGAGGAGAGATAGTCAGAAAATAAAGCCCTCTCTCTCTCTTTCGCAT 1379
Db 88 CTTTCAATGCTGCTGTAGTATATACAGAAAACAGTTGACTTTTGTATTTTGACCTC 147

QY 1380 CTATACATACGAATTCATATATACGTTTCATTGCAATCATCTTTTGTATATATCTCAAAAAG 1439
Db 148 ATATCTTACCTTGCTGCTAAATTTATTTATTTAGTCTAGAAAATTTCTTTAGATCTTTTGG 207

QY 1440 ATCTCTTAGTTCGCAATAGTCAAACTTCAAATTTATAGCCCTTATATTTT 1492
Db 208 ATTTTTCACACTGATAAATTTATTTAATTTGCAAAATAAATATATCATGTTTATTTCT 260

RESULT 8
US-11-011-332A-151/c
; Sequence 151, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dima
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwope, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SU
; TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011,332A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
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; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 151
; LENGTH: 28536
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-151

Query Match      2.7%; Score 42.6; DB 12; Length 28536;
Best Local Similarity 46.7%; Pred. No. 46;
Matches 204; Conservative 0; Mismatches 229; Indels 4; Gaps 2;

QY 1101 TAAAGATATAAAACATAAAGCTGATTCAAATACTCGAATTCGACACCAATTCATTTGCGCTTA 1160
Db 19689 TAACCATTAACCAATTCGGAATCTAACACCAAAATTTCTCACAAAAAATTTATCTTA 19630

QY 1161 CACCAAAAATTTTATTAATCAATTTAGTGAATATGATAAAAAATGATAATGAAAAATAGTA 1220
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QY 1221 TTTTACTGATTTGGCTTCGCATTCGACACCGCCCAAT--TTACATGACGAATTTGTTA 1278
Db 19569 TCCCAATTTATTTAAACTCAATTTCTTAATAAACCTAATCAATTAATAAACATATAAA 19510

QY 1279 TATATAATAGACCACTTATCCGAATTTGTGAATAAAATTTGATCAATCAAAATTTAGTGGAGGA 1338
Db 19509 TACAAATCTCAAAACCTCAITTTTAACTACAAAAATAAATCTCCAAATCACAACAAATATA 19450

QY 1339 AGATAGTCAGAAATAAAGCCTTCTCTCTCTCTCTCTCTCGCATCTATACATACGATTTTCATA 1398
Db 19449 AAATAAACTAAAAAACACGCCTTAAACCTTCT--TTTCAATCTCTTAAAAATAAACTCTATA 19392

QY 1399 TATAGCTTTCTTGGATCATCTTTTGATATATCTCAAAAAGATCTCTTAGTTGCAAAATA 1458
Db 19391 AATCTTTAAAAATTTATTTTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 19332

QY 1459 GTCAAAATCTTCAAAATTTATAGCCTTTTATATTTTTCACGATTTTCTGAAACCTCTTTTATA 1518
Db 19331 ATAAAAAAAATAATATAATAATAATACTTACACCAAAACGCAATCTTTTCT 19272

QY 1519 TCAGCACCGTTAATGCT 1535
Db 19271 TTTATATATTTTCATTTCT 19255

RESULT 9
US-11-011-332A-155/c
; Sequence 155, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimrich, Inko
; APPLICANT: Rujan, Tamas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dima
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwope, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKERS FOR PREDICTION OF TREATMENT RESPONSE AND/OR SU
; TITLE OF INVENTION: BREAST CELL PROLIFERATIVE DISORDER PATIENTS
; FILE REFERENCE: 47675-99
; CURRENT APPLICATION NUMBER: US/11/011,332A
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 06:36:26 ; Search time 1353.36 Seconds
(without alignments)
9587.015 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1569	100.0	1569	7	US-10-041-018-1
2	1008	64.2	1008	6	US-10-369-493-46181
3	1008	64.2	1008	7	US-10-450-941-5
4	568.6	36.2	599	9	US-10-487-901-363
5	114	7.3	1395	6	US-10-189-268-4
6	114	7.3	1692	3	US-09-814-353-21762
7	114	7.3	2534	7	US-10-041-018-3
8	113.6	7.2	2529	3	US-09-925-302-171
9	113.6	7.2	2529	3	US-09-925-302-171
10	102.6	6.5	1044	6	US-10-369-493-36092
11	99.6	6.3	1888	8	US-10-357-930-25125
12	90.6	5.8	1284	6	US-10-369-493-27908
13	87.5	5.6	51001	6	US-10-189-268-11
14	84.2	5.4	2210	10	US-11-097-143-9632
15	84.2	5.4	2222	7	US-10-041-018-21
16	70.6	4.5	1882	7	US-10-001-192A-14
17	68.8	4.4	554	3	US-09-969-034-1324
18	68.4	4.4	716	3	US-09-969-034-1924
19	65.6	4.2	593	3	US-09-969-034-1488
20	62.4	4.0	1843	7	US-10-041-018-5
21	60	3.8	399	8	US-10-357-930-49920
22	58.6	3.7	1095	7	US-10-282-122A-40388
23	58.6	3.7	1364	6	US-10-369-493-36669

ALIGNMENTS

RESULT 1

US-10-041-018-1

; Sequence 1, Application US/10041018

; Publication No. US20040072323A1

; GENERAL INFORMATION:

; APPLICANT: Matsuda, Seiichi P.T.

; APPLICANT: Hart, Elizabeth A.

; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism

; FILE REFERENCE: P02080051/10025547

; CURRENT APPLICATION NUMBER: US/10/041, 018

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: US 60/259880

; PRIOR FILING DATE: 2001-01-05

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; LENGTH: 1569

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-10-041-018-1

Query Match 100.0%; Score 1569; DB 7; Length 1569;

Best Local Similarity 100.0%; Pred. No. 0;

Mismatches 0; Indels 0; Gaps 0;

Matches 1569; Conservative 0;

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DB 1 AATATTACATATAGATAGGCAAGCCGCGCATTTTCATCTGAAAGGTAACCTTCTATT 60

QY 61 ATTATAGTGTATCCAAAGTTCCACGCTCCAGCATAGCAAGAAATACGTTGTTTCAT 120

DB 61 ATTATAGTGTATCCAAAGTTCCACGCTCCAGCATAGCAAGAAATACGTTGTTTCAT 120

QY 121 ATGTTATGCTGATCATTTGTTATGCTTACTACCATTTTTTTCGCTTCGCTTCTTTT 180

DB 121 ATGTTATGCTGATCATTTGTTATGCTTACTACCATTTTTTTCGCTTCGCTTCTTTT 180

QY 181 GACGTTTTTTGAAGCAAAAAGTCAAGACAGATGTCTTACAAAACCATGTAGGC 240

DB 181 GACGTTTTTTGAAGCAAAAAGTCAAGACAGATGTCTTACAAAACCATGTAGGC 240

QY 241 TCATTTTCAAGAGAGTCTTAATAGAAAGACAAAGAGTTTACGAGTCTGGAATCA 300

DB 241 TCATTTTCAAGAGAGTCTTAATAGAAAGAGTCTTAATAGAAAGAGTCTGGAATCA 300

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DB 301 ATGAGGCCAAGATAGATGAGCTGATCAATATGATCTCTTTGGTCCAGCCAAATGAA 360

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Db 301 ATGGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 1440
QY 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 1500
Db 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 1500
QY 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCCAAAAGACAGCTGGCCATAGTT 1560
Db 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCCAAAAGACAGCTGGCCATAGTT 1560
QY 481 TCGCAAAATTTGAGCTCTTGCATATTTCCAGCCTTTTAAATCGACATATAGAGTAAT 540
Db 481 TCGCAAAATTTGAGCTCTTGCATATTTCCAGCCTTTTAAATCGACATATAGAGTAAT 540
QY 541 GCTCCCTTCGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTATA 600
Db 541 GCTCCCTTCGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTATA 600
QY 601 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 660
Db 601 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 660
QY 661 GAGCCTTTCTATCATATTTGATGATGATTTTCAACGAGAAATGATCAATCTACATAGG 720
Db 661 GAGCCTTTCTATCATATTTGATGATGATTTTCAACGAGAAATGATCAATCTACATAGG 720
QY 721 GGCAAGGCTTGGATATATCTGAGAGACTTTCTGCCTGAAATCATACTACTCAGAGAG 780
Db 721 GGCAAGGCTTGGATATATCTGAGAGACTTTCTGCCTGAAATCATACTACTCAGAGAG 780
QY 781 ATGATTTTCAATATGTTTATGAATAAAACAGGCGGCTTTTTCAGATTAACGTTGAGACTC 840
Db 781 ATGATTTTCAATATGTTTATGAATAAAACAGGCGGCTTTTTCAGATTAACGTTGAGACTC 840
QY 841 ATGGAGCCCTGCTCTCTTCTCACACACGCGGCTTGGTGGTTCCTTTTCATTAATCTT 900
Db 841 ATGGAGCCCTGCTCTCTTCTCACACACGCGGCTTGGTGGTTCCTTTTCATTAATCTT 900
QY 901 CTGGGTATTTATTTATCAGATTAAGATGATTAATCTGAAATTTGAAAGATTTCAAATGTCC 960
Db 901 CTGGGTATTTATTTATCAGATTAAGATGATTAATCTGAAATTTGAAAGATTTCAAATGTCC 960
QY 961 AGCGAAAAAGGCTTCTGCTGAGGACATTAACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Db 961 AGCGAAAAAGGCTTCTGCTGAGGACATTAACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 1020
QY 1021 GCGCTTAACTTCACTAAAACGAAAGGTCAAACTGAGCAACACAACTGAAATTTCTAAGAAAT 1080
Db 1021 GCGCTTAACTTCACTAAAACGAAAGGTCAAACTGAGCAACACAACTGAAATTTCTAAGAAAT 1080
QY 1081 CTCCTGTCGAGGACAAATGATTAAGATATAAACTAAAGCTGATTCGAAATCTGGAATTC 1140
Db 1081 CTCCTGTCGAGGACAAATGATTAAGATATAAACTAAAGCTGATTCGAAATCTGGAATTC 1140
QY 1141 GACACCAATTCATTTGCGCTTACACCAAAAATTTTATTAATCAATAGTGAATATGATAAAA 1200
Db 1141 GACACCAATTCATTTGCGCTTACACCAAAAATTTTATTAATCAATAGTGAATATGATAAAA 1200
QY 1201 AATGATAATGAATAATAGTATTTTACCTGATTTGGCTTCGCATTTCCGACACCGCCCAAT 1260
Db 1201 AATGATAATGAATAATAGTATTTTACCTGATTTGGCTTCGCATTTCCGACACCGCCCAAT 1260
QY 1261 TTACATGACGAATTTGTTATATATATAGACCACTTATCGAAATTTGAAATTAATTTGATC 1320
Db 1261 TTACATGACGAATTTGTTATATATATATAGACCACTTATCGAAATTTGAAATTAATTTGATC 1320
QY 1321 AATCAAAATTTAGTGAGGAAGATAGTCAGAAAAATAAGCCCTTCTCTCTCTTTTCCCATC 1380
Db 1321 AATCAAAATTTAGTGAGGAAGATAGTCAGAAAAATAAGCCCTTCTCTCTCTTTTCCCATC 1380
QY 1381 TATACATAGATTTTCATATATAGCTTTTCATTCGATCATCTTTTGTATATATCTCAGGAG 1440

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Db 1381 TATACATAGATTTTCATATATAGCTTTCAATGATCACTTTTGTATATCTCAAAAAGA 1440
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Db 1501 TTCTGAAACTCTTTTTTATCAGACACCGTTAAATGCTAGCGGTTACTGTCAAATGCGCGTA 1560
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Db 1561 AATTGCGGA 1569

RESULT 2
US-10-369-493-46181
; Sequence 46181, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46181
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-46181

Query Match 64.2%; Score 1008; DB 6; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.5e-229;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 ATGGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 360
Db 1 ATGGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 60
QY 361 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 420
Db 61 AGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGGCAAGAACTTTAGACTA 120
QY 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTTGGCCAAAGACAGCTGGCCATAGTT 480
Db 121 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTTGGCCAAAGACAGCTGGCCATAGTT 180
QY 481 TCGCAAAATTTGAGCTCTTGCATATTTCCAGCCTTTTAAATCGACATATAGAGTAAT 540
Db 181 TCGCAAAATTTGAGCTCTTGCATATTTCCAGCCTTTTAAATCGACATATAGAGTAAT 240
QY 541 GCTCCCTTCGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTATA 600
Db 241 GCTCCCTTCGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCACTATA 300
QY 601 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 660
Db 301 AACACCGCAAAATTAATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAAAA 360
QY 661 GAGCCTTTCTATCATATTTGATGATGATTTTCAACGAGAAATGATCAATCTACATAGG 720
Db 361 GAGCCTTTCTATCATATTTGATGATGATTTTCAACGAGAAATGATCAATCTACATAGG 420
QY 721 GGCAAGGCTTGGATATATCTGAGAGACTTTCTGCCTGAAATCATACTACTCAGAGAG 780

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Db 421 GGCAAGGCTTGGATATATACCTGAGAGACTTTCTGCTGAAATCATACCTACTCAGGAG 480
Qy 781 ATGTATTTGAATATGTTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 840
Db 481 ATGTATTTGAATATGTTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 540
Qy 841 ATGGAAGCGCTGCTCTCTCTCTCAACACGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 900
Db 541 ATGGAAGCGCTGCTCTCTCTCTCAACACGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 600
Qy 901 CTGGGTATTTATCATAGATTAGAGATGATTTGAAATTTGAAAGATTTCCAAATGTC 960
Db 601 CTGGGTATTTATCATAGATTAGAGATGATTTGAAATTTGAAAGATTTCCAAATGTC 660
Qy 961 AGCGAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Db 661 AGCGAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 720
Qy 1021 GCCCTTAACTTCACTAAAAAGAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAAAT 1080
Db 721 GCCCTTAACTTCACTAAAAAGAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAAAT 780
Qy 1081 CTCCTGTGAGGACAAAGTATAAGATATAAACTAAAGCTGATTCAAATCTGGAATTC 1140
Db 781 CTCCTGTGAGGACAAAGTATAAGATATAAACTAAAGCTGATTCAAATCTGGAATTC 840
Qy 1141 GACACCAATTCATTTGGCTCACCCAAAAATTTTATTAATCAATTTAGTGAATATGATAAA 1200
Db 841 GACACCAATTCATTTGGCTCACCCAAAAATTTTATTAATCAATTTAGTGAATATGATAAA 900
Qy 1201 AATGATAATGAAATAAGTATTTTACCTGATTTGGCTTCGATTCGACACCGCCACCAAT 1260
Db 901 AATGATAATGAAATAAGTATTTTACCTGATTTGGCTTCGATTTGGCTTCGACACCGCCACCAAT 960
Qy 1261 TTACATGACGAATTTGTTATATATAATAGACCACTTATCCGAATTTGGA 1308
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RESULT 3

US-10-450-941-5
; Sequence 5, Application US/10450941
; Publication No. US20040063182A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: A METHOD OF PRODUCING PRENYLALCOHOL
; FILE REFERENCE: PH-144PCT
; CURRENT APPLICATION NUMBER: US/10/450,941
; CURRENT FILING DATE: 2003-06-18
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP2000-401701
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP2000-403067
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP2001-282978
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1005)
US-10-450-941-5

Query Match 64.2%; Score 1008; DB 7; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.5e-229; Indels 0; Gaps 0;
Matches 1008; Conservative 0; Mismatches 0;
Qy 301 ATGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 360
Db 1 ATGAGGCCAAGATAGATGAGCTGATCAATAATGATCCTGTTGGTCCAGCCAAATGAA 60

Qy 361 AGCTTGTATTTCAAAACCTTTAATACATCCCTTTTGAACCTGSCAAGAACTTTAGACTA 420
Db 61 AGCTTGTATTTCAAAACCTTTAATACATCCCTTTTGAACCTGSCAAGAACTTTAGACTA 120
Qy 421 AATTTAATAGTTCAAAATTAACAGAGTTATGAAATTTGCCAAAGACAGCTGGCCATAGTT 480
Db 121 AATTTAATAGTTCAAAATTAACAGAGTTATGAAATTTGCCAAAGACAGCTGGCCATAGTT 180
Qy 481 TCCCAATTTGCTGAGCTCTTGCATNAATCCAGCCTTTTAATCCAGCATATAGAGATAAT 540
Db 181 TCCCAATTTGCTGAGCTCTTGCATNAATCCAGCCTTTTAATCCAGCATATAGAGATAAT 240
Qy 541 GCTCCCTTGAAGAGGGGACAGACCACTTCTCACTTAATCTTGGTGTAACCTCCACTATA 600
Db 241 GCTCCCTTGAAGAGGGGACAGACCACTTCTCACTTAATCTTGGTGTAACCTCCACTATA 300
Qy 601 AACACCGCAAAATTAATATGTAATTTTTCAGAGCCATGCACTTGTATCGCAGCTAACCCAAAA 660
Db 301 AACACCGCAAAATTAATATGTAATTTTTCAGAGCCATGCACTTGTATCGCAGCTAACCCAAAA 360
Qy 661 GAGCCTTTGTATCATTAATTTGATTAACGATTTTCAACGAAGATTTGATCAATCTACATAGG 720
Db 361 GAGCCTTTGTATCATTAATTTGATTAACGATTTTCAACGAAGATTTGATCAATCTACATAGG 420
Qy 721 GGACAAAGGCTTGGATATATACCTGAGAGACTTTCTGCTCGAAATCATACCTACTCAGGAG 780
Db 421 GGACAAAGGCTTGGATATATACCTGAGAGACTTTCTGCTCGAAATCATACCTACTCAGGAG 480
Qy 781 ATGTATTTGAATATGTTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 840
Db 481 ATGTATTTGAATATGTTTATGAATAAACAAGCGGCGCTTTTTCAGATTAAAGTTGAGACTC 540
Qy 841 ATGGAAGCGCTGCTCTCTCTCAACACGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 900
Db 541 ATGGAAGCGCTGCTCTCTCTCAACACGCGCAATTCGTTGGTTCCTTTTCATATAATCTT 600
Qy 901 CTGGGTATTTATCATAGATTAGAGATGATTTGAAATTTGAAAGATTTCCAAATGTC 960
Db 601 CTGGGTATTTATCATAGATTAGAGATGATTTGAAATTTGAAAGATTTCCAAATGTC 660
Qy 961 AGCGAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Db 661 AGCGAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 720
Qy 1021 GCCCTTAACTTCACTAAAAAGAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAAAT 1080
Db 721 GCCCTTAACTTCACTAAAAAGAAAGGTCAAACTGAGCAACCAATGAAATTTCTAAGAAAT 780
Qy 1081 CTCCTGTGAGGACAAAGTATAAGATATAAACTAAAGCTGATTCAAATCTGGAATTC 1140
Db 781 CTCCTGTGAGGACAAAGTATAAGATATAAACTAAAGCTGATTCAAATCTGGAATTC 840
Qy 1141 GACACCAATTCATTTGGCTCACCCAAAAATTTTATTAATCAATTTAGTGAATATGATAAA 1200
Db 841 GACACCAATTCATTTGGCTCACCCAAAAATTTTATTAATCAATTTAGTGAATATGATAAA 900
Qy 1201 AATGATAATGAAATAAGTATTTTACCTGATTTGGCTTCGATTCGACACCGCCACCAAT 1260
Db 901 AATGATAATGAAATAAGTATTTTACCTGATTTGGCTTCGATTCGACACCGCCACCAAT 960
Qy 1261 TTACATGACGAATTTGTTATATATAATAGACCACTTATCCGAATTTGGA 1308
Db 961 TTACATGACGAATTTGTTATATATAATAGACCACTTATCCGAATTTGGA 1008

RESULT 4

US-10-487-901-363
; Sequence 363, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David

; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-0852
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 363
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-487-901-363

Query Match 36.2%; Score 568.6; DB 9; Length 599;
Best Local Similarity 98.5%; Pred. No. 6e-125;
Matches 574; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 299 CAATGAGGCCAAGATAGAGCTGATCAATAATGATCCTGTGTTGGTCCAGCCAAAATG 358
Db 17 CCATGAGGCCAACAATACATGAGCTGATCAATAATGATCCTGTGTTGGTCCAGCCAAAATG 76
QY 359 AAAGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGCGAAGAACTTTAGAC 418
Db 77 AAAGCTTGATTTCAAAACCTTATATACATCCTTTTGAACCTGCGAAGAACTTTAGAC 136
QY 419 TAAATTTAATAGTTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATAG 478
Db 137 TAAATTTAATAGTTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATAG 196
QY 479 TTTTCGCAAAATTTGTAGCTCTTGATATATTCAGAGCCATGCAACTTTGATCGCAGCTAACCCACAA 658
Db 197 TTTTCGCAAAATTTGTAGCTCTTGATATATTCAGAGCCATGCAACTTTGATCGCAGCTAACCCACAA 256
QY 539 ATGCTCCCTTGAGAGGGGACAGACCTTCTACCTTAATCTTCGGTGTACCTCCACTA 598
Db 257 ATGCTCCCTTGAGAGGGGACAGACCTTCTACCTTAATCTTCGGTGTACCTCCACTA 316
QY 599 TAAACACCGCAAAATATATATGTTTTCAGAGCCATGCAACTTTGATCGCAGCTAACCCACAA 658
Db 317 TAAACACCGCAAAATATATATGTTTTCAGAGCCATGCAACTTTGATCGCAGCTAACCCACAA 376
QY 659 AAGAGCTTTGTATATCAATAATTTGATTTAAGTTTCAACGAGAAATTTGATCAATCTACATA 718
Db 377 AAGAGCTTTGTATATCAATAATTTGATTTAAGTTTCAACGAGAAATTTGATCAATCTACATA 436
QY 719 GGGGCAAGCTTGGATATATATCTGAGAGACTTTCTGCTGAAATCATCTACTCAGG 778
Db 437 GGGGCAAGCTTGGATATATATCTGAGAGACTTTCTGCTGAAATCATCTACTCAGG 496
QY 779 AGATGTATTTGAATATGTTTATGAATAAAACAGGCGGCTTTTTCAGATTAACCTTTGAGAC 838
Db 497 AGATGTATTTGAATATGTTTATGAATAAAACAGGCGGCTTTTTCAGATTAACCTTTGAGAC 556
QY 839 TCATGGAAGCGTGTCTCTTCTCTACACAGGCGCAATTCGTT 881
Db 557 TCATGGAACACTGTCTCTCTCTACACAGGCGCAATTCGTT 599

RESULT 5
US-10-189-268-4
; Sequence 4, Application US/10189268
; Publication No. US20040005570A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF GERANYLGRANVL DIPHOSPHATE SYNTHASE 1 EXP
; FILE REFERENCE: PTS-0021
; CURRENT APPLICATION NUMBER: US/10/189,268
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 4
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(1072)
US-10-189-268-4

Query Match 7.3%; Score 114; DB 6; Length 1395;
Best Local Similarity 52.1%; Pred. No. 2e-16;
Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;
QY 359 AAAGCTTGATTTCAAAACCTTATATATCAATCCTTTTGAACCTGCGAAGAACTTTAGAC 418
Db 195 AAAGAATTTCTCTAGAACCTTATAATACTTACTTCAGTTACCAGGTAACAAGTGAGAA 254
QY 419 TAAATTTAATAGTTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATAG 478
Db 255 CCAAACTTTTCAGGCAATTTAATCATTTGGCTGAAAGTTCCAGAGGCAAGCTACAGATTA 314
QY 479 TTTTCGCAAAATTTGTAGCTCTTGATATATTCAGAGCCCTTTTAAATCGACGATATAGAGATA 538
Db 315 TTAATTTGAAGTGCAGAGAAATGTTGCATATATGCCAGTTTACTCATCGATGATATTTGAAGACA 374
QY 539 ATGCTCCCTTGAGAGGGGACAGACCTTCTCACTTAATCTTCGGTGTACCTCCACTA 598
Db 375 ACTCAAAACCTCGACGCTGCTTTTCCAGTGGCCACAGACATCTATGGAATCCCATCTGTCA 434
QY 599 TAAACACCGCAAAATTTATATGTTTTCAGAGCCATGCAACTTTGATCGCAGCTAACCCACAA 658
Db 435 TCAATTTCTGCCAATTTACGTGTATTTCTTTGGCTTTGGAGAAAGTCT----- 479
QY 659 AAGAGCTTTGTATCATATTTTGTATTCAGATTTTCAACGAGAAATTTGATCAATCTACATA 718
Db 480 TAACTCTTGATCACCCAGATGCGAGTGAAGCTTTTACCCGCGAGCTTTTGGAACTCCATC 539
QY 719 GGGGCAAGCTTGGATATATATCTGAGAGACTTTCTGCTGAAATCATCTACTCAGG 778
Db 540 AGGGACAGGCTAGATATTTTCTGGAGGGA-----TAAATTACACTTGTCCCACTGAAG 593
QY 779 AGATGTATTTGAATATGTTTATGAATAAAACAGGCGGCTTTTTCAGATTAACCTTTGAGAC 838
Db 594 AAGAATATAAAGCTATGGTGTGCGAGAAACAGGTGGACTGTGTTGATTTAGCGTAGGTC 653
QY 839 TCATGGAAGCGTGTCTCTCTCTCACACAGGCGCAATTCGTTGGTTCCTTTTCATAAATC 898
Db 654 TCATGCGATTGTTCTCTGATTACAAAGAGATTTTAAACCGCTACTT-----AATA 704
QY 899 TTTCTGGTATTAATTTATCAGATTAGAGATGATTCTTGAATTTGAAAGATTTTCCAAATGT 958
Db 705 CACTTGGGCTCTTTTCCAAATTTAGGATGATTATGCTAATCTACACTCCAAAGATATA 764
QY 959 CCAGCGAAAGAGCTTTGCTGAGGACATTTACAGAGGGAAGTTATCTTTTCCCATCGTC 1018
Db 765 GTGAAACAAAGATTTTGTGGAAGATCTGACAGAGGGAAGTTCTCATTTTCTTACTATTTC 824
QY 1019 ACGCCCTT 1026
Db 825 ATGCTATT 832

RESULT 6
US-09-814-353-21762
; Sequence 21762, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:

; APPLICANT: Lee, John
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
 ; FILE REFERENCES: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/211,940
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 22037
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21762
 ; LENGTH: 1692
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1, 1692
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-21762

Query Match 7.3%; Score 114; DB 3; Length 1692;
 Best Local Similarity 52.1%; Pred. No. 2.2e-16;
 Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;
 359 AAAGCTTGATTTCAAAACCTTATAATCAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAG 418
 280 AAAGAATCTTCTAGAACCTTATAATATCTTACTTCTAGTTACAGGTAACAGAGTGAGAA 339
 419 TAAATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAG 478
 340 CCAAACTTTACAGGCAATTAATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 399
 479 TTTGCGAAATTTGTAGCTCTTGCAATTAATTCAGGCTTTTAAATCGACGATATAGAATA 538
 400 TTATTGAAGTGACAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGACA 459
 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAACTTTCGGTGTACCCCTCCACTA 598
 460 ACTCAAACTCCGACGTGGCTTTCCAGTGGCCACAGCATCTATGGAATCCCATCTGTCA 519
 599 TAAACACCGCAAAATTAATATGTTATTTTCAGAGCCATGCAACTTTGTATCGCAGCTAACCAAA 658
 520 TCAATTTCTGCAATTAAGTTATTTCTTCTGGCTTGGAGAAAGTCT-----564
 659 AAGAGCTTTGTATCATAATTTGATTAAGTTTTCAGAGGAAATTTGATCAATCTACATA 718
 565 TAAACCTTTGATCACTCCAGATGCAAGCTTTTACCCGCCAGCTTTTGGAACTCCATC 624
 719 GGGGACAAGGCTTGGATATATCTTGGAGAGACTTTCTGCTGCTGAAATCATACCTACTCAGG 778
 625 AGGACAAGGCTTAGATATTTACTTGGAGGGA-----TAAATACCTTTGTCCTCCACTGAAG 678
 779 AGATGTTATTTGAATATGTTTATGAATAAAACAGCGGCCCTTTTTCAGATTAACGTTGAGAC 838
 679 AAGNATAAAGCTATGCTGCTGCAGAAACAGAGTGAGCTGTTGGATTAGCAGTAGGTC 738
 839 TCATGGAAGCGCTGTCTCTTCTTCCCTCACACACCGGCCAATTCGTTGGTTTCTTTCATAATC 898
 739 TCATGCAAGTTGTTCTCTCTGATTACAAAGAGATTAAACACCGCTACTT-----AATA 789

899 TTCTGGGTATTTATCTATCAGATAGATGATTACTTGAATTTGAAAGATTTCCAAATGT 958
 790 CATTGGGCTCTTTTCCAAATTTAGGATGATTATGCTATCTACACTCCAAAGATATA 849
 959 CCAGCGAAAAAGGCTTTGCTGAGGACATTAACAGAGGGAAGTTATCTTTCCCATCGTCC 1018
 850 GTGAAAAACAAAGTTTTGTGAAGATCTGACAGAGGGAAGTTCTCATTTCTTACTATTTC 909
 1019 ACGCCCTT 1026
 910 ATGCTATT 917
 RESULT 7
 US-10-041-018-3
 ; Sequence 3, Application US/10041018
 ; Publication No. US20040072323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuda, Seiichi P.T.
 ; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
 ; FILE REFERENCE: P02080US1/10025547
 ; CURRENT APPLICATION NUMBER: US/10/041,018
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: US 60/259880
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 2534
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-041-018-3

Query Match 7.3%; Score 114; DB 7; Length 2534;
 Best Local Similarity 52.1%; Pred. No. 2.7e-16;
 Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;
 359 AAAGCTTGATTTCAAAACCTTATAATCAGATGATTGAATTTGCCAAAGACAGCTGGCCATAG 418
 258 AAAGAATCTTCTAGAACCTTATAATATCTTACTTCTAGTTACAGGTAACAGAGTGAGAA 317
 419 TAAATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACAGCTGGCCATAG 478
 318 CCAAACTTTACAGGCAATTAATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATTA 377
 479 TTTGCGAAATTTGTAGCTCTTGCAATTAATTCAGGCTTTTAAATCGACGATATAGAATA 538
 378 TTATTGAAGTGACAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGACA 437
 539 ATGCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAACTTTCGGTGTACCCCTCCACTA 598
 438 ACTCAAACTCCGACGTGGCTTTCCAGTGGCCACAGCATCTATGGAATCCCATCTGTCA 497
 599 TAAACACCGCAAAATTAATATGTTATTTTCAGAGCCATGCAACTTTGTATCGCAGCTAACCAAA 658
 498 TCAATTTCTGCAATTAAGTTATTTCTTCTGGCTTGGAGAAAGTCT-----542
 659 AAGAGCTTTGTATCATAATTTGATTAAGTTTTCAGAGGAAATTTGATCAATCTACATA 718
 543 TAAACCTTTGATCACTCCAGATGCAAGCTTTTACCCGCCAGCTTTTGGAACTCCATC 602
 719 GGGGACAAGGCTTGGATATATCTTGGAGAGACTTTCTGCTGCTGAAATCATACCTACTCAGG 778
 603 AGGACAAGGCTTAGATATTTACTTGGAGGGA-----TAAATACCTTTGTCCTCCACTGAAG 656
 779 AGATGTTATTTGAATATGTTTATGAATAAAACAGCGGCCCTTTTTCAGATTAACGTTGAGAC 838
 657 AAGNATAAAGCTATGCTGCTGCAGAAACAGAGTGAGCTGTTGGATTAGCAGTAGGTC 716
 839 TCATGGAAGCGCTGTCTCTTCTTCCCTCACACACCGGCCAATTCGTTGGTTTCTTTCATAATC 898
 717 TCATGCAAGTTGTTCTCTCTGATTACAAAGAGATTAAACACCGCTACTT-----AATA 767

Qy	899	TTCTGGGTATTA	TATTA	TACAGATTA	GAGATTA	CTTGA	ATTTG	GAAGA	ATTTCC	AAATGT	958	
Db	768	CAC	TGGGCTCT	TTTTT	CCAAAT	TAGG	GATTA	TGCT	TAATCT	CACATCC	AAAGATATA	827
Qy	959	CCAGCGAAA	AAGGCT	TTTGCT	GAGGAC	ATTAC	GAGAGG	GGAG	CTTATCT	TTTTCC	CAATCGTCC	1018
Db	828	GTGAAA	ACAAAG	TTTTT	TGTGA	AGATCT	GCAGAG	GGGAA	AGTTCT	CAATTT	CTCTACTATTC	887
Qy	1019	ACGCCCTT	1026									
Db	888	ATGCTATT	895									

```

RESULT 8
US-09-925-302-171
; Sequence 171, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-171

```

Query Match	7.2%	Score 113.6;	DB 3;	Length 2529;
Best Local Similarity	51.9%;	Pred. No. 3.4e-16;		
Matches	347;	Conservative 1;	Mismatches 290;	Indels 30; Gaps 3;
Qy	359	AAAGCTGATTTCAAAACCTTATAATCACATCCTCTTTTGAAACCTGGCAAGAACTTTAGAC	418	
Db	246	AAAGAAATCTCTTAGAACCTTATAATACCTTACTTACAGTTACCAAGGTAAACAAGTAGAA	305	
Qy	419	TAAATTTAAATAGTTCAAATTAACAGAGTTATGAATTTGCCCAAGACCGACTGGCCCATAG	478	
Db	306	CCAACTTTCACAGGCATTTAATCATTTGGCTGAAAGTTCCAGAGGACACAGCTACAGATTA	365	
Qy	479	TTTCGCAAAATTTGTAGCTCTTGCAATAATCCAGCCCTTTTAAATCGACGATATAGAAGATA	538	
Db	366	TTATTGAAGTCACAGAAATGTTGCATAATGTCAGTTTACTCATCGATGATATTGAAGACA	425	
Qy	539	ATGCTCCCTTGAGAAAGGGACAGACACTTCTCACTTAATCTTCGGTGTACCCCTCCACTA	598	
Db	426	ACTCAAAACTCCGACGTGGCTTTCCAGTGGGCCACAGCATCTATGGAATCCCATCTGTCA	485	
Qy	599	TAAACACGCGAAATATATATGTTATTTTCAGAGCCATGCAACTTGTATCGCAGCTAACCAA	658	
Db	486	TCAATCTGCCAATTTACGTGTATTTCTTGGCTTGGAGAAAGTCT-----	530	
Qy	659	AAGAGCCTTTGTATCATAAATTTGATTTACGATTTTCAACGAAGAAATGATCAATCTACATA	718	
Db	531	TAAACCTTGATCACCCGATGCGAGTGAAGCTTTTACCGCCAGCTTTTGGAACTCCATC	590	
Qy	719	GGGACAAAGGCTTGGATATATACCTGGAGAGACTTTCTTCGCTGAAATCATACCTACTCAGG	778	
Db	591	AGGACAAAGGCTAGATATTTACTGGAGGGA-----TAATTACACTTGTCCCACTGAAG	644	
Qy	779	AGATGTATTTGAAATATGGTTATGATTAATAACAGGGGCCCTTTTTCAGATTAACGTTGAGAC	838	
Db	645	AAGAATATAAAGCTATGGTGTCTGAGAAACAGGTGGACTGTTTGGATATTAGCAGTAGTCT	704	
Qy	839	TCATGGAAAGCGCTGTCTCTTCTCCTCACACACCGGCCATTCGTTGGTTCCTTTTCAATAATC	898	

Db	705	TCATG	CAAGTTGTTCTCTCTGATTACAAAGAAAGATTTAAACCGCTACTTT-----AATA	755
Qy	899	TTCTGGG	TATTATTATTCAGATTAGAGATGATTACTTGAATTTGAAAGATTTCCAAATGT	958
Db	756	CAC	TGGGCTCTTTTTTCCAAATTAGGAGATGATTATGCTAATCTACACTCCAAAGAATATA	815
Qy	959	CCAGC	GAAGGCTTTGTCTGAGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCC	1018
Db	816	GTG	AAAAACAAAAGTTTGTGTAAGATCTGCACAGAGGGAAGTTCTCATTTCTACTATTC	875
Qy	1019	ACGCC	CTT 1026	
Db	876	ATG	CTATT 883	

RESULT 9

US-09-925-302-171

; Sequence 171, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 171

; LENGTH: 2529

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-302-171

Query Match	7.2%;	Score 113.6;	DB 3;	Length 2529;
Best Local Similarity	51.9%;	Pred. No. 3.4e-16;		
Matches 347;	Conservative 1;	Mismatches 290;	Indels 30;	Gaps 37;
Qy	359	AAAGCTTGATTTCAAAACCTTTATAATCACATCCTTTTGAACCTCGGCAAGAACTTTAGAC	418	
Db	246	AAAGAAATCTCTAGAACCTTATAAAATACATTACTTCAGTTACCAAGGTAAACAAGTGAA	305	
Qy	419	TAAATTTAATAGTTCAAATTTAAACAGAGTTATGAATTTGCCCAAGACAGAGTCGGCCATAG	478	
Db	306	CCAAACTTTCACAGGCATTTAAATCATTTGGCTGAAAGTTCCAGAGGACAAGGCTACAGATT	365	
Qy	479	TTTCGCAAAATGTTGAGCTCTTGATATAATTCACGCCCTTTTAATCGACGATATAGAAGATA	538	
Db	366	TTATTGAAGTCACAGAAATGTTGCTATATGCCAGTTTACTCATCGATGATATCGAGACA	425	
Qy	539	ATGCTCCCTTGAGAAAGGGGACAGACCACTCTCTCACTTAACTTCGCTGTACCCCTCCACT	598	
Db	426	ACTCAAAACTCCGACGTGGGCTTTCCAGTGGGCCACAGCATCTATGGAATCCCATCTGTCA	485	
Qy	599	TAAACCGCGAAATTTATGTATTTTCAGAGCCATGCAACTTTGATCGCAGCTAACCCACAA	658	
Db	486	TCAATTCGCCAATTACGTGATTTTCCTTGGCTTGGAGAAAGTCT-----	530	
Qy	659	AAGAGCCTTTGTATCATATAATTTGATTACGATTTTTCACGAAGAATTGATCAATCTACATA	718	
Db	531	TAAACCTTGTATCACCCAGATGCAGTGAAGCTTTTTTACCGCGCAGCTTTTGGAACTCCATC	590	
Qy	719	GGGACACAGGCTTCGATATATACCTGGAGAGACTTTCTGCGCTGAAATCATACTCACTCAGG	778	
Db	591	AGGGACAAGGCTAGATATTTACTCGHAGGA-----TAATTACACTTGTCCCACTGAAG	644	
Qy	779	AGATGTATTTGAAATATCGTTTATGAATTAACAACAGCGGCGCTTTTCAGATTAAACGTTGAGAC	838	
Db	645	AAGAATATAAAGCTATCGTGTCGAGAAAAACAGGTGGACTGTTTGGATTTAGCAGTAGGTC	704	

QY 839 TCATGGAAGCGCTGCTCTCTCTCTCACACCGCCCATTCGTTGGTTCTTTTCATTAATC 898
 DB 705 TCATGCAAGTGTCTCTGATTACAAAGATTAAACCGCTACTT-----ATA 755
 QY 899 TTCTGGGTATATTTATCAGATAGAGATGATTACTTTGAATTTGAAGATTTCCAAATGT 958
 DB 756 CACTTGGGCTCTTTTCCAAATTAGGATGATTATGCTAATCTACACTCCAAAGATATA 815
 QY 959 CCAGCGAAAAGCGCTTGGCTGAGGACATTACAGAGGGGAAGTTATCTTTCCCATCGTCC 1018
 DB 816 GTGAAACAAAGTTTGTGTGAAGATCTGACAGAGGGAAGTTCTCATTTCTACTATTTC 875
 QY 1019 ACGCCCTT 1026
 DB 876 ATGCTATT 883
 RESULT 10
 ; Sequence 36092, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 36092
 ; LENGTH: 1044
 ; TYPE: DNA
 ; ORGANISM: Aspergillus nidulans
 ; US-10-369-493-36092
 Query Match 6.5%; Score 102.6; DB 6; Length 1044;
 Best Local Similarity 49.9%; Pred. No. 9.2e-14;
 Matches 363; Conservative 0; Mismatches 334; Indels 30; Gaps 3;
 QY 300 AATGAGGCCAAGATGATGAGCTGATCAATAATGATCTGTTGGTCCAGCCAAATGA 359
 DB 153 AAATCAGTCAAGTCTCGACGGGCAAAATACAAAGATGGGAAATGGTCCCAAGAGATGA 212
 QY 360 AAGCTTGATTTCAAAACCTTATATACATCTTTTGAACCTGGCAAGAACTTTAGACT 419
 DB 213 GGAGGTGATCATGGTCCGTACGACTACATGCTGCAACACCCGGGGAAGGACCTGCGACG 272
 QY 420 AAATTTAATGATTTCAAAATTAACAGATGTTGAATTTGGCCCAAGACCAGCTGCCCATAGT 479
 DB 273 GCAGATGATCAACGCTTTTAAAGTATGTTGAAGTGGCATCTGAGAGCTGGCCATCAT 332
 QY 480 TTCCGAAATTTGAGCTCTTGATCAATATTCACGCTTTTAAATCGACGATATAGAAGATA 539
 DB 333 CACCAAGATAGTGGCTATGCTCCATACCGCTTCATTATTGATCGACGACGTCGAAGACAA 392
 QY 540 TGCTCCCTTCAGAGAGGGGACAGACCACTTCTCATTAACTTTGGTGTACCTCCCATAT 599
 DB 393 CTCTCTTCTCCGGGAGGAATTCGGTTCGCACATAGCATCTATGGCACCGCGCAGACGAT 452
 QY 600 AAACACGCAAAATATATGATTTTTCAGAGCCATGCAACTTGTATCGCAGCTTAACCAAA 659
 DB 453 CAATTCGGCAAACTACGTTTACTTCTCGCCCTCCAGGAGGTGCAAAAACCTGAAGATCC 512
 QY 660 AGAGCCCTTTGATCATAAATTTGATACGATTTTCAACGAGAAATTTGATCAATCTACATAG 719
 DB 513 GGCAGCTATCGAC-----ATATACGTTCCAGGAGCTGCTGTAATTTTACACAG 557

QY 720 GGCACAAGGCTTCGATATATCTGGAGAGACTTTTCGCCCTGAAATCATCATCTACTCAGGA 779
 DB 558 AGGCAAGGATGATGATCTGTTCTGGCGAGACAGCTCATTGT-----CCAACCGAGA 611
 QY 780 GATGATTTGAATATGTTATGAATAAAACAGCGGCTTTTTCAGATTAACGTTGAGACT 839
 DB 612 TGAATACTTGGAGATGGTGGGCAACAAGACTCGGAGGTTTGTTCGGGCTAGCTGTGAAAT 671
 QY 840 CATGGAGCGCTCTCTCTCTCTCACACCGGCCATTCTGTTGGTTCCTTTTCATAAATCT 899
 DB 672 GATGCAAG-----CTGAAAAGCAGCACTGGAAGGACTGTGTGGCCCTTGTGAATGT 722
 QY 900 TCTGGGTATTATTATCAGATTAGAGATGATTCTTGAATTTTGAAGATTTTCCAAATGTC 959
 DB 723 TTGGGACTGCTCTTTTCAGATATGCGACGACTATCTCAATTTATCCGACGAGGATATAC 782
 QY 960 CAGCGAAAAGGCTTTGCTGAGGACATTTACAGAGGGGAAGTTATCTTTTCCCATCGTCCA 1019
 DB 783 CCAGAACAAAGGCTCTGTGGAAGACCTCACAGAGGGCAAAATTTTCATTTCCCATTAATCCA 842
 QY 1020 CGCCCTT 1026
 DB 843 CAGCAT 849
 RESULT 11
 ; US-10-357-930-25125
 ; Sequence 25125, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endese, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 25125
 ; LENGTH: 1888
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 2, 1888
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-357-930-25125
 Query Match 6.3%; Score 99.6; DB 8; Length 1888;
 Best Local Similarity 51.8%; Pred. No. 6.4e-13;
 Matches 346; Conservative 0; Mismatches 289; Indels 33; Gaps 4;
 QY 359 AAGCTTGATTTTCAAAACCTTATTAATCAGATCTTTTGAACCTGGCAAGAACTTAGAC 418
 DB 479 AAAGAATTTCTTCTAGAACCTTATAAATCTTACTTTCAGTTTACCAGGTAAACAAAGTGAGAA 538

QY 419 TAAATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCCCAAGACCAAGCTGGCCATAG 478
 Db 539 CCAAACTTTTCAGAGCATTTAATCATTTGGCTGAAAGTTCCAGAGGACAAAGCTACAGATT 598
 QY 479 TTTTCGCAATTTGAGCTTTGCAATAATCCAGCCCTTTTAAATCGACGATATAGAGATA 538
 Db 599 TTATTGAAGTGACAGAAATGTTGCAATAATGCCAGTTTACTCATCGATGATATGGAAGACA 658
 QY 539 ATGCTCCCTTGAGAGGGGACAGACACCTTCTCACTTAATCTTGGGTGACCTCCACTA 598
 Db 659 ACTCAAACTCCGAGCTGCTTTCCAGTGGCCCAACAGCATCTATGAAATCCCATCTGTCA 718
 QY 599 TAAACACCCCAATATATATGATTTTCAGAGCAATGCAACTTGTATGCGAGCTAAACACAA 658
 Db 719 TCAATTTCTGCCAATACGTGTATTTCTTGGCTTGGAGAAAGTCT----- 763
 QY 659 AAGAGCCTTTGTATCATATAATTTGATTTACGATTTTCAACGAAGATTTGATCAATCTACATA 718
 Db 764 TAAACCTTGCATCACCAGATGAGTGAAGCTTTTACCGCCAGCTTTTGGAACTCCATC 823
 QY 719 GGGGCAAGCTTTGGATATATATCTGAGAGACTTTCTGCTGAAATCATACCTACTCAGG 778
 Db 824 AGGCAACAGCTTAGATATTTACTGGAGGA-----TAATTACACTTGTCCCACTGAAG 877
 QY 779 AGATGATTTGAATATGTTTATGAATAAACAAGGCGGCTTTTCAGATTAAAGTTGAGAC 838
 Db 878 AAGAATATAAAGCTATGTTGCTGCAGAAACAGGTGACTGTTGGATTAGCAGTAGGTC 937
 QY 839 TCATGGAAGCGCTGCTCTCTCTCACACCAGGCCATTTGTTGTTCTTTTCATAAATC 898
 Db 938 TCATGAGTTGTTCTCTGATTAACAAGAGATTTAAACCGCTACTTAATACACTTGGGC 997
 QY 899 TTTCTGGTATTATTATCAGATTAGAGATGATTAATCTTGAATTTGAAAGATTTCCAAATGT 958
 Db 998 TC-----TTTCCAAATTAGGATGATTAATCT-ACACTCCAAAGATAT 1045
 QY 959 CCAGCGAAAGCGTTTGTGAGGACATTAACAGAGGGAAGTTATCTTTTCCATCGTCC 1018
 Db 1046 AGTGAACAAAGTTTGTGAAGATCTGACAGAGGAAAGTTCTCATTTCTCTACTATTTC 1105
 QY 1019 ACGCCCTT 1026
 Db 1106 ATGCTATT 1113

RESULT 12
 US-10-369-493-27908
 ; Sequence 27908, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 27908
 ; LENGTH: 1284
 ; TYPE: DNA
 ; ORGANISM: Neurospora crassa
 US-10-369-493-27908

Query Match 5.8%; Score 90.6; DB 6; Length 1284;
 Best Local Similarity 49.6%; Pred. No. 7.4e-11;
 Matches 339; Conservative 0; Mismatches 314; Indels 30; Gaps 3;

QY 343 TGGTCCAGCCAAAATGAAGCTTGTGATTTCAAAAACCTTATAATACATCTCTTTTGAACCT 402
 Db 361 TGGTCCGAAGAGAGAGAGAGGTTCTGACGGGTCTTACGACTATCTCAACGGGACCGG 420
 QY 403 GCGAAGACTTTAGACTAAATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGGCCAAA 462
 Db 421 GGCAGAGACATCCGATCGCAGATGTCAGGCTTCGACGCTGCGCTTGTATGTGCGGTCC 480
 QY 463 GACCAGCTGGCCATAGTTTGCAAAATTTGTAGCTCTTGCATAAATTCAGACCTTTTAAATC 522
 Db 481 GAAAGCTCGAGTGCATCAACAAAGTCATCAGCATGCTACACAGACCTCTTGTCTCGTC 540
 QY 523 GACGATATAGAGATAATGCTCCCTTGAGAAAGGAGACAGACCTTCTCACTTAATCTTTC 582
 Db 541 GACGACGTGGAAGACAAACAGCGTCTTGGCGCCGCGCTTCCCTGTGCGCCACCTCCATCTTC 600
 QY 583 GGTGTACCTCCACTATAAACACCGCAATATATATGTAATTTCCAGAGCCATGCAACTTGA 642
 Db 601 GGCATCCCGCAGACCATCAACACGTCACACTACGTGTATTTCTACGCGTGCAGAAATTG 660
 QY 643 TCGCAGCTAAACCAAAAAGAGCGCTTTTGTATCATATAATTTGATTAACGATTTTCAACGAAGAA 702
 Db 661 CAAAAGCTCAAGA-----ACCCAAAGCGCTCAGCATTTTCTCTGAAGAA 705
 QY 703 TTGATCAATCTATACATAGGGGACAGGCTTTGGATATATATCTGAGAGACATTTCTGCTCGAA 762
 Db 706 CTGCTCAACTGCACCGGGCCAGGGAATGGACCTCTTTTGGCGTGACACGCT-----C 759
 QY 763 ATCATACCTACTCAGGAGATGTAATTTGAATATGTTTGAATATAAACAAGCGCGCTTTTC 822
 Db 760 ACTCTCCGACGGGAGACGACTACCTAGAGATGGTATCCAAACAGACAGCGCGTCTGTTTC 819
 QY 823 AGATTAAGCTTCAGACTCATGGAAGCGTGTCTCTCTCTCACACACCGGCCATTCGTTG 882
 Db 820 CGTTGGGAATCAAGCTGATGACGCGGAGTCCGCTCGCGGTGAGCTGC----- 870
 QY 883 GTTCTTTTCATAAAATCTTCTGGGTATTAATTAATCAGATTAGAGATGATTACTTTGAATTTG 942
 Db 871 GTCCGCTCGTCAACATCATCGACTGATCTTCCAGATCGCGAGCATTATCATATCTG 930
 QY 943 AAAGATTTCCAAATCTCCAGCGAAAAGCGTTTGTGAGGACATTACAGAGGGGAAGTTA 1002
 Db 931 TGGAAACCGCGAGTACACGGCCAAACAGGGCATGTGCGAGGACCTGACGGAGGCAAGTTTC 990
 QY 1003 TCTTTTCCCATCGTCCAGCGCCT 1025
 Db 991 AGTTTCCCGTGCATCCACAGCAT 1013

RESULT 13
 US-10-189-268-11
 ; Sequence 11, Application US/10189268
 ; Publication No. US20040005570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Kenneth W. Doble
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF GERANYLGERANYL DIPHOSPHATE SYNTHASE 1 EXPR
 ; FILE REFERENCE: PTS-0021
 ; CURRENT APPLICATION NUMBER: US/10/189,268
 ; CURRENT FILING DATE: 2002-07-02
 ; NUMBER OF SEQ ID NOS: 131
 ; SEQ ID NO 11
 ; LENGTH: 51001
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1331-1430, 34714-34813
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-189-268-11


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; SEQ ID NO 21
; LENGTH: 2222
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-041-018-21

Query Match      5.4%; Score 84.2; DB 7; Length 2222;
Best Local Similarity 50.5%; Pred. No. 3.3e-09;
Matches 330; Conservative 0; Mismatches 293; Indels 30; Gaps 4;

QY 374 AACCTTATAATCACATCCCTTTTGAAACCTGGCAAGAACTTTAGACTAAATTTAATAGTTC 433
Db 372 AGCCCTTTACATACACACAGATTCTTGGCAAGCAATTCGCTCTGAGTTGGCCTTGG 431
QY 434 AAATTAACAGAGTTATGAATTTGCCCAAGACCAAGCAGCTGGCCATAGTTTCGCAAAATTTGG 493
Db 432 CCTTCAATCACTGGTTGCTCATACCGGGGCAAAAGTTGGCGCAGATCGGAGACATTTGTGC 491
QY 494 AGCTCTTGCAATATCCAGCCTTTTAAATCGACGATATAGAGATATGCTCCCTTGAGAA 553
Db 492 AGATGCTGCACAAATTCAGTTTGCTCAATTGATGATATGAAGACAATTCGATCCTTCGCA 551
QY 554 GGGGACAGACCACTTCTCACTTAATCTCGGTGTACCTCCACTATAAAACACGCAAAAT 613
Db 552 GAGGTGTCGGCGGCGATTCCATCTACGGCGTGGCCAGCACCATAAATGGGCCAACT 611
QY 614 ATATGATTTTCAGAGCCATGCAACTTTGTATCGCAGCTAACCAAAAGAGCCCTTTGTATC 673
Db 612 ATGCACCTCTTCTGGCGCTGGAGAAGGTGCAGCAGCTGGATCATCCGGAGGCT----- 664
QY 674 ATAAATTTGATTAGATTTTCAACGAGAATTTGATCAATCTACATAGGGGACAGGCTTGG 733
Db 665 -----ACCAAGGTGTACCCGAAATTTGCTGGAGCTGCACCGTGGACAGGGCATGG 716
QY 734 ATATATACTGGAGAGACTTCTGCCTGAAATCATACTACTCAGGAGATGTATTTGAATA 793
Db 717 AGATCTATTGGCGCGACAGCTT-----CACGTGTCATCCGAGTCGGATTACAAGCTGA 770
QY 794 TGGTTATGAATAAAACAGGCGGCTTTTCAGATTAAAGTTGAGACTCATGGAGCGCTGT 853
Db 771 TGACTGTGGCAAAACTGGCGGCTCTTTATGCTGGCCATTCGCCTTATGCA---GCTGT 827
QY 854 CTCCTTCTCTCACACGCGGCAATTCGTTGTTCTTTCATTAATCTTCTGGGTATTTATTT 913
Db 828 TCAGCTCCAACAAAGGAGGACTATTCGAAG-----TTGACGGCTATATTGGGCTGTACT 881
QY 914 ATCAGATTAGAGATGATTACTTCAATTTGAAAGATTTCCAAATGTCCAGCGAAAAAGGCT 973
Db 882 TTCAGATACGCGACGACTATTGCAATCTGAGTCTGAAGAGTACACGGAGNACAAGAGCT 941
QY 974 TTGCTCAGGACATTAACAGAGGGGAAGTTATCTTTTCCCATCGTCCACGCGCCTT 1026
Db 942 TCGCCGAGGACTTGACGGAGGGCAAGTTCCGCTTCCCGGTAATCCATCCATCGGGTT 994
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Job time : 1358.36 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 06:52:12 ; Search time 163.758 Seconds
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Title: US-10-041-018-22

Perfect score: 1720

Sequence: 1 MEAKIDELINNDPVWSSQNE.....DTATNLHDELLYIDHLSEL 335

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1720	100.0	1005	2	US-08-761-344-1
2	1720	100.0	1569	2	US-08-761-344-3
3	574	33.4	903	2	US-08-469-665-1
4	574	33.4	903	2	US-09-038-596-1
5	574	33.4	903	6	PCT-US95-00421-1
6	538	31.3	1882	3	US-09-091-725-14
7	310.5	18.1	1664976	3	US-08-916-421B-1
8	310.5	18.1	1664976	3	US-09-692-570-1
9	242.5	14.1	924	3	US-09-543-681A-1736

10	234.5	13.6	993	2	US-08-705-377-4	Sequence 4, Appli
11	234.5	13.6	993	2	US-09-052-962-4	Sequence 4, Appli
12	234.5	13.6	993	2	US-09-053-068-4	Sequence 4, Appli
13	233	13.5	1026	3	US-09-252-991A-4877	Sequence 4877, Ap
14	232	13.5	498	3	US-09-248-796A-3882	Sequence 3882, Ap
15	230.5	13.4	993	2	US-08-705-377-3	Sequence 3, Appli
16	230.5	13.4	993	2	US-08-705-377-6	Sequence 3, Appli
17	230.5	13.4	993	2	US-09-052-962-3	Sequence 3, Appli
18	230.5	13.4	993	2	US-09-052-962-6	Sequence 3, Appli
19	230.5	13.4	993	2	US-09-053-068-3	Sequence 3, Appli
20	230.5	13.4	993	2	US-09-053-068-6	Sequence 3, Appli
21	229.5	13.3	993	2	US-08-705-377-5	Sequence 5, Appli
22	229.5	13.3	993	2	US-09-052-962-5	Sequence 5, Appli
23	228.5	13.3	993	2	US-09-053-068-5	Sequence 5, Appli
24	228.5	13.3	993	2	US-08-410-167A-1	Sequence 1, Appli
25	228.5	13.3	993	2	US-08-705-377-1	Sequence 1, Appli
26	228.5	13.3	993	2	US-09-052-962-1	Sequence 1, Appli
27	228.5	13.3	993	2	US-09-053-068-1	Sequence 1, Appli
28	228.5	13.3	993	2	US-08-898-560-2	Sequence 2, Appli
29	228.5	13.3	993	3	US-09-101-126-2	Sequence 2, Appli
30	227	13.2	1029	3	US-09-489-039A-6482	Sequence 6482, Ap
31	225.5	13.1	978	3	US-09-217-609A-4	Sequence 4, Appli
32	225.5	13.1	978	3	US-08-873-235B-4	Sequence 4, Appli
33	225.5	13.1	2451	3	US-09-217-609A-21	Sequence 21, Appl
34	225.5	13.1	2451	3	US-08-873-235B-21	Sequence 21, Appl
35	225	13.1	993	2	US-08-705-377-2	Sequence 2, Appli
36	225	13.1	993	2	US-09-052-962-2	Sequence 2, Appli
37	225	13.1	993	2	US-09-053-068-2	Sequence 2, Appli
38	221.5	12.9	993	3	US-09-252-991A-4908	Sequence 4908, Ap
39	221.5	12.9	1023	3	US-09-543-681A-1606	Sequence 1606, Ap
40	211.5	12.3	717	3	US-09-252-991A-4822	Sequence 4822, Ap
41	211.5	12.3	1350	3	US-09-266-965-80	Sequence 80, Appl
42	211.5	12.3	18034	3	US-09-266-965-75	Sequence 75, Appl
43	210.5	12.2	1219	3	US-09-025-819-28	Sequence 28, Appl
44	210.5	12.2	1219	3	US-09-808-126-28	Sequence 28, Appl
45	210.5	12.2	1219	3	US-09-803-951-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-08-761-344-1

; Sequence 1, Application US/08761344

; Patent No. 5912154

; GENERAL INFORMATION:

; APPLICANT: Ferro-No. 5912154ick, Susan

; APPLICANT: Jiang, Yu

; TITLE OF INVENTION: GERANYLGERANYL DIPHOSPHATE SYNTHASE

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheridan Ross P.C.

; STREET: 1700 Lincoln Street

; CITY: Denver

; STATE: CO

; COUNTRY: U.S.A.

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/761,344

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Connell, Gary J.

; REGISTRATION NUMBER: 30,020

; REFERENCE/DOCKET NUMBER: 3161-14

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 303/863-9700

; TELEFAX: 303/862-0223

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1005 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1005
US-08-761-344-1

Alignment Scores:
Pred. No.: 1,08e-194 Length: 1005
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-041-018-22 (1-335) x US-08-761-344-1 (1-1005)

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QY 21 SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
DB 61 AGCTTGATTCAAAACCTTATAATCATCATCTCTTTTGAAACCTGGCAAGAACTTTAGACTA 120
QY 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnIleAlaIleVal 60
DB 121 AATTTAATAGTTCAAATTAACAGAGTATGAATTTGCCCAAGACGAGCTGGCCATAGTT 180
QY 61 SerGlnIleValGlnLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn 80
DB 181 TGCAGAAATTTTGAGCTCTTGCAATATTCAGCTTTTAATCGACATATAGAGATAT 240
QY 81 AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
DB 241 GCTCCCTTCAGAAAGGGGACAGACCACTTCTCACTTAATCTCGGTGATCCCTCCACTATA 300
QY 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLys 120
DB 301 AACACCGCAATATATATGATTTTCAGAGCATGCACTTTGTATCGCAGTAACCAACAAA 360
QY 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
DB 361 GAGCCTTTGTATCATAAATTTGATTTCGATTTTCAAGAAAGATGTGATCAATCTACATAGG 420
QY 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
DB 421 GGACAGGCTTGGATATATCTGGAGAGACTTCTGCCTGAAATCATACCTACTCAGGAG 480
QY 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
DB 481 ATGTATTTGAATATGTTATGAATAAAACAGGGCGCTTTTCAGATTAACGTTGAGACTC 540
QY 181 MetGluAlaLeuSerProSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
DB 541 ATGGAAAGCGCTGTCTCTCCCTCACACCGGCAATTCGTGGTTCCTTTCATAAAATCT 600
QY 201 LeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
DB 601 CTGGGTATTTATTCAGATTAGAGATGATTACTTGAATTTGAAAGATTTCCAAATGTCC 660
QY 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
DB 661 AGCGAAAAAGGCTTTCTCGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 720
QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
DB 721 GCCCTTAATCTTCAATAAAGAAAGGTCAAACTGAGCAACACATGAAATTTCAAGAAAT 780

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1005 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1005
US-08-761-344-1

Alignment Scores:
Pred. No.: 2.16e-194 Length: 1569
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-041-018-22 (1-335) x US-08-761-344-3 (1-1569)

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DB 301 ATGGAGCCCAAGATAGATGCTGATCAATATATGCTCTGGTTCGACGCAAAATGAA 360
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Qy 41 AsnLeuLeuValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 421 AATTAAATAGTTCAAATTAACAGAGTTATGAATTTGCCCAAAGACCGCTGGCCATAGTT 480
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Qy 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrLys 120
Db 601 AACACCCGCAATATATATGTTATTCAGAGCCATGCAACTTGTATCGAGCTTAACCAAAA 660
Qy 121 GluProLeuTyrHisAsnLeuLeuThrIlePheAsnGluLeuLeuLeuLeuLeuLeuLeu 140
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Db 721 GGACAAGCTTTGGATATATATCTCGAGAGACTTTCTGCTGAAATCATACCTACTCAGGAG 780
Qy 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuLeuLeuLeuLeu 180
Db 781 ATGTATTGTAATATGTTATGAATTAACACAGCGCGCTTTTCAGATTAACGTTGAGACTC 840
Qy 181 MetGluAlaLeuSerProSerSerHisGlyHisSerLeuValProPheIleAsnLeu 200
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Qy 201 LeuGlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 901 CTGGGTATTTATCATCAGATTAGAGATGATTACTTTGAATTTGAAGATTTCCAAATGTC 960
Qy 221 SerGlnLysGlyPheAlaGluAspIleThrGluLysLeuSerPheProIleValHis 240
Db 961 AGCGAAAAGAGCTTTGCTGAGGACATTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Qy 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
Db 1021 GCCCTTAACCTTCACTAAACGAAAGGTCAAACTGAGCAACACAAATGAATTTCTAAGAA 1080
Qy 261 LeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGluPhe 280
Db 1081 CTCTGTTGAGGCAAGTATAGATATATAAATAAAGCTGATTCAATACTGGAATTC 1140
Qy 281 AspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 1141 GACACCAATTCATTTGGCTCAACCAAAATTTTATTAATCAATAGTGAATATGATAAAA 1200
Qy 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 1201 AATGATTAATGAAATAATAGTATTACCTCGATTGGCTTCGATTCGACACCGCCACCAAT 1260
Qy 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 1261 TTACATGACGAAATTTGTTATATATATATAGACCATTTATCCGAATG 1305

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RESULT 3

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US-08-469-665-1
; Sequence 1, Application US/08469665
; Patent No. 5786193
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; US-08-469-665-1

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Alignment Scores:

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Pred. No.: 1,81e-58 Length: 903
Score: 574.00 Matches: 127
Percent Similarity: 57.6% Conservative: 55
Best Local Similarity: 40.2% Mismatches: 104
Query Match: 33.4% Indels: 30
DB: 2 Gaps: 8

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US-10-041-018-22 (1-335) x US-08-469-665-1 (1-903)

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Qy 20 GluSerLeuLeuSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArg 39
Db 25 CAAAGAAATTTCTAGAACCTTATAAATACTTCACTTACAGTTTACCAGGTAAACAAGTGA 84
Qy 40 LeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIle 59
Db 85 ACCAACTTTCACAGGCAATTTATCATTTGGCTGAAAGTTCCAGAGGACAAGCTACAGATT 144
Qy 60 ValSerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuLeuLeuLeuLeuLeuLeu 79
Db 145 ATTATTGAAGTGACAGAAATGTTGCATAATGCCAGTTTACTCATCGATGATATTGAAGAC 204
Qy 80 AsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSerThr 99
Db 205 AACTCAAAACTCCGAGCGTGGCTTTCCAGTGGCCGACAGCATCTATGGAATCCCATCTGTC 264
Qy 100 IleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThr 119
Db 265 ATCAATTCGCCAAATACGTGTATTTCTTGGCTTGGAGAAAGTC-----TTAACCCCTT 318
Qy 120 LysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluLeuLeuLeuLeuLeuHis 139
Db 319 GATCACCCA-----GATGCAGTAGAAGCTTTTACCAGCCAGCTTTTGGAACTCCAT 369
Qy 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGln 159
Db 370 CAGGACGACAGGCTTAGATATTTACTTGGAGGAT-----AATTACACTTGTGCCCACTGAA 423

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QY 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
Db 424 GAAGAATAAAGCTATGTGCTGCAGAAACACAGGTGGACTGTTGGATTACAGTAGGT 483
QY 180 LeuMetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheLeuAsn 199
Db 484 CTCATGCAGTTGTC-----TCTGATTACAAAGAGATTAAACCGCTACTTAAT 534
QY 200 LeuLeuGlyIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMet 219
Db 535 ACACCTGGGCTCTTTTCCAAATTAGGGATGATTATGCTTAATCTACACATCCAAAGAAATAT 594
QY 220 SerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleVal 239
Db 595 AGTGAACAAAGAGTTGGGTGAAGATCTGCAGAGGGAAGTTCATCTTCTACTATT 654
QY 240 HisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArg 259
Db 655 CATGCTATT-----TGTCAAGTCTGAAAGCACCCAGGTGCAGAT 696
QY 260 IleLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGlu 279
Db 697 ATCTTGGCCAGAGAACACATAGATATAAAAAAATACTGTGTACATTCTTTGAG 756
QY 280 PheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIle 299
Db 757 ---GATGTAGTTCTGGGAATACACTCGTAATACCTTTAAAGAGCTT----- 801
QY 300 LysAsnAspGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThr 319
Db 802 -----GAGCTAAA-----GCCATAACAGATTGATGCACGT 834
QY 320 AsnLeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 835 GGTGGGAACCTGAGCTAGTACCTTAGTAAACACACTTAAGTAAGATG 882

RESULT 4
US-09-038-596-1
; Sequence 1, Application US/09038596
; Patent No. 5928924
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,596
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-09-038-596-1

Alignment Scores:
Pred. No.: 1,81e-58 Length: 903
Score: 574.00 Matches: 127
Percent Similarity: 57.6% Conservatives: 55
Best Local Similarity: 40.2% Mismatches: 104
Query Match: 33.4% Indels: 30
DB: 2 Gaps: 8

US-10-041-018-22 (1-335) x US-09-038-596-1 (1-903)
QY 20 GluSerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArg 39
Db 25 CAAGAAGATCTTCTAGAACCTTATAATATCTTACTTACGTTCAGTTCACAGGTAAACAAAGTGAGA 84
QY 40 LeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIle 59
Db 85 ACCAACTTTCACAGGCATTTAATCATTTGGCTGGAAGTTCCAGAGGACAAAGCTACAGATT 144
QY 60 ValSerGlnIleValGlnLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAsp 79
Db 145 ATATTGAAGTCACAGAAATGTTGCATAATGCCAGTTACTCATCATCATGATATTGAAGAC 204
QY 80 AsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThr 99
Db 205 AACTCAAAACTCCGACGTGGCTTCCAGTGGGCCACAGCATCTATGGAATCCCATCTGTC 264
QY 100 IleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThr 119
Db 265 ATCAATTCGCCAATTCAGTGTATTCTTGGCTGGGAGAAAGTC-----TTAACCCCTT 318
QY 120 LysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHis 139
Db 319 GATCACCCA-----GATGCAGTGAAGCTTTTACCCTCCAGCTTTTGGAACTCCAT 369
QY 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGln 159
Db 370 CAGGACCAAGGCTAGATATTTACTGGAGGAT-----AATTACACTTTGTCCCACTGAA 423
QY 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
Db 424 GAAGAATAAAGCTATGTGCTGCAGAAACACAGGTGGAGTGTGTTGGATTAGCAGTAGGT 483
QY 180 LeuMetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheIleAsn 199
Db 484 CTCATGCAGTTGTC-----TCTGATTACAAAGAGATTAAACCGCTACTTAAT 534
QY 200 LeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGlnMet 219
Db 535 ACACCTGGGCTCTTTTCCAAATTAGGGATGATTATGCTTAATCTACACATCCAAAGAAATAT 594
QY 220 SerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleVal 239
Db 595 AGTGAACAAAGAGTTGGGTGAAGATCTGCAGAGGGAAGTTCATCTTCTACTATT 654
QY 240 HisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArg 259
Db 655 CATGCTATT-----TGTCAAGTCTGGAAGCACCCAGGTGCAGAAAT 696
QY 260 IleLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGlu 279
Db 697 ATCTTGGCCAGAGAACACATAGATATAAAAAAATACTGTGTACATTCTTTGAG 756
QY 280 PheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIle 299

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725

FILING DATE: 23-DEC-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA: EP 95203620.0

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: EP 96200943.7

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: E. Victor Donahue

REGISTRATION NUMBER: 35,492

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1882 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Phaffia rhodozyma

FEATURE:

NAME/KEY: CDS

LOCATION: 82..1212

OTHER INFORMATION: /product= "PRcrte"

US-09-091-725-14

Alignment Scores:

Pred. No.: 1,08e-53 Length: 1882
Score: 538.00 Matches: 117
Percent Similarity: 52.1% Conservative: 79
Best Local Similarity: 31.1% Mismatches: 110
Query Match: 31.3% Indels: 70
DB: 3 Gaps: 7

US-10-041-018-22 (1-335) x US-09-091-725-14 (1-1882)

QY 15 TrpSerSerGlnAsnGluSerLeuLeuSerLysProTyrAsnHisIleLeuLeuLysPro 34

DB 121 TTACTCTCAGAGATATCGTGTCTTGAACCGTATCACTTACCTAGGAAGAACCCCT 180

QY 35 GlyLysAsnPhaArgLeuAsnLeuIleValGlnIleAsnArgValMetAsnProLys 54

DB 181 CGAAAGAAATTCGATCACAACTCATCGAGGCTTCAACTATTGGTTGGATGTCAAGAAG 240

QY 55 AspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIle 74

DB 241 GAGGATCTCGAGTCTATCCAGAACGTTGTTGGCATGCTACATACCGCTAGCTTATTAATG 300

QY 75 AspAspIleGluAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePhe 94

DB 301 GACGATGTGGAGATTCATCGGTCTTCAGCGGTGGGTGCGCTGTGGCCCATCTAATTATAC 360

QY 95 GlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal 114

DB 361 GGGATTCGCGACACAATAACATCGCAACTAGCTACTTCTGCGCTTATCAAGAGATC 420

QY 114 ----- 114

DB 421 TTCAAGCTTCGCCCAACACCGATACCCATGCCTGTAATTCTCTTCATCTGCTTGCCT 480

QY 114 ----- 114

DB 481 CAATCATCGTCTCTCTGCACT 540

QY 115 -----SerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIle 130

DB 541 TCAACTCTCTAAATTCGAGATTCGGTCTCTCGAAAGATACGCTAT-----CTTGATAAAGTG 594

QY 131 PheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpAsp 150

DB 595 ATCAGACAGAGATGCTTTCCCTCATAGAGCGCAGGCTGAGCTATTCGAGAGAT 654

QY 151 PheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThr 170

DB 655 AGCTCTG-----ACGTGCTCTAGCAGAGAGGAATATGTGAAAATGGTCTTGGAAAGACG 708

QY 171 GlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHisHis 190

DB 709 CGAGGTTTCTCCGTATAGCGGTTCAGATTGATGATGGCA-----AAGTCAGAAATGT 759

QY 191 GlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAspAsp 210

DB 760 GACATAGACTTTGTCCAGCTTGTCAACTTGTATCAATATATCTTCAGATCAGGGAAGAC 819

QY 211 TyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThr 230

DB 820 TATATGAACCTTCAGTCTTCAGTATGCCCATATAAGAAATTTGCAGAGGACCTCACA 879

QY 231 GluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln 250

DB 880 GAAGGAAATTCAGTTTCCCACTATCCACTCGATTCCATCCCAACCCCTCATCG----- 933

QY 251 ThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIle 270

DB 934 -----AGACTCGTCTCATCAATACGTTGCGAGAGAAATCGACCTCTCTCTGAGATC 981

QY 271 LysLeuLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsn 290

DB 982 CTTACCACTGTGTAACTACATGCGCAGAGAAACCCACTCATTCGAATATATCTCAGGAA 1041

QY 291 PheIleAsnGlnLeuValAsnMetIleLysAsnAsp----- 302

DB 1042 GTCTCAACACCTTGTCTGAGTGCACCTCGAGAGAGAACTAGGAGGCTTCAAGGAGAGTTC 1101

QY 303 -----AsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThr 319

DB 1102 GCAGAAAGTAACTCAAGGATGGATCTTGGAGACGTAGATTTCGAGAGAAAGAGGGGGAAG 1161

QY 320 AsnLeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335

DB 1162 AACGTC-----AAATTGGAACGATCTCTGAAAAGAGCTAGCCGATATC 1203

RESULT 7

US-08-916-421B-1

; Sequence 1, Application US/08916421B

; Patent No. 6503729

; GENERAL INFORMATION:

; APPLICANT: Bult et al.

; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus

; Patent No. 6503729

; TITLE OF INVENTION: jannaschii

; FILE REFERENCE: PB275

; CURRENT APPLICATION NUMBER: US/08/916,421B

; PRIOR FILING DATE: 1997-08-22

; CURRENT FILING DATE: 1996-08-22

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1664976

; TYPE: DNA

; ORGANISM: Methanococcus jannaschii

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (28222)..(28222)

; OTHER INFORMATION: n equals a, t, c, or g

; NAME/KEY: misc feature

; LOCATION: (28257)..(28258)

; OTHER INFORMATION: n equals a, t, c, or g

; NAME/KEY: misc feature

; LOCATION: (84773)..(84773)

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NAME/KEY: misc feature
LOCATION: (1470091)..
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NAME/KEY: misc feature
LOCATION: (1569020)..
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature

; LOCATION: (1664854) ..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Alignment Scores:

Pred. No.: 4 63e-22 Length: 1664976
Score: 310.50 Matches: 94
Percent Similarity: 44.1% Conservative: 56
Best Local Similarity: 27.6% Mismatches: 119
Query Match: 18.1% Indels: 71
DB: 3 Gaps: 11

US-10-041-018-22 (1-335) x US-08-916-421B-1 (1-1664976)

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QY 4 LysIleAspGlu-----LeuIleAsnAspProValTrpSerSerGlnAsn 19
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Db 688576 AAAATGTGAAGAAATTAAGACTTATGTAGATAAAGAT----- 688614
QY 20 GluSerLeuIleSerIysProTyrAsn-----HisIleLeuLeuIysProGlyLys 36
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Db 688615 -----GATAAACCTATATAACGCGTCAAAACATCTCTATTGCTCGAGGAAAG 688662
QY 37 AsnPheArgLeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGln 56
   |||||
Db 688663 AGAATTAGGCCATATTTAACTGTAGTA-----ACTTATATGTTGAAGAAAGACGAT 688713
QY 57 LeuAlaIleVal-----SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeu 73
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Db 688714 ATTGAGGAGGTTTTCGACCGCTGCTGCAGTAGAGTTAATTCAACACTACACCTTAATA 688773
QY 74 IleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIle 93
   |||||
Db 688774 CATGATGACATTTATGACAAATGATGAGAGGAGGAGGAAACCAACAGCTTCATGTTGTC 688833
QY 94 PheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeu 113
   |||||
Db 688834 TATGGAGAGCCATGGCTATCTTAGCTGGAGATTTATTATATGCTTAAAGCTTTTGAAGCA 688893
QY 114 ValSerGlnLeuThrThrIysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGlu 133
   |||||
Db 688894 GTTTCAGAATAAAGATAATAAAGAGCT---CATGAAGTTTAAATAATCCTATCAAAA 688950
QY 134 GluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuPro 153
   |||||
Db 688951 GCATGTTGTAGGTTTGTGAAGGCGGAGCAATGGCAATGGAATTTCAAAACTAC----- 689004
QY 154 GluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeu 173
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Db 689005 -----TATCCTACATGGAAGAACTACTAGATATGATTAGAAAAAAGACAGAGCTTTA 689058
QY 174 PheArgLeuThrLeuArgLeuMetGluAlaLeuSerPro---SerSerHisGlyHis 192
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Db 689059 TTAGAGGCTTCGTGGGAATTCGGGCTGTTATGGCTGATTGTAATGAAGAGAAAGGGA 689118
QY 193 SerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspTyrLeu 212
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Db 689119 GCATTTAAAGAGATATGCAAAAAGAAATTCGATTAACCTTTTCAAAATACAGGATGTTTAA 689178
QY 213 AsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThrGluGly 232
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Db 689179 GATTTAATTGGGACACGAAAAAGTTAGTAGCCAGTTGGAGTGATATAGAGAAAGT 689238
QY 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGlu 252
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Db 689239 AAAAGACAAATAATGTTATCCAGCC----- 689265
QY 253 GlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeu 272
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Db 689266 -----CTAAAAACATTCGATGAAGATAAAGAA 689295
QY 273 LysLeuIleGlnIleLeu----- 278
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Db 689296 AGATTATTGGAAATTTTAGGAAATAAATAATGTTAGGATGAAGAAATTAAGAACCAATT 689355
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QY 279 GluPheAspThrAsnSerIeuAlaTyrThrIysAsnPheIleAsnGlnIeuValAsnMet 298
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Db 689356 GAGATATTAAAGCCTTCAATTGAATATGCAAAAGAACTTATGAAACAAAAAACTGAAGAA 689415
QY 299 IleLys-----AsnAspAsnGluAsnLysTyrIeuProAspLeuAla 312
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RESULT 8

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US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
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; LOCATION: (779676)..(779676)
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; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
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; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
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; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g

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Alignment Scores:

Pred. No.:	4,638-22	Length:	1664976
Score:	310.50	Matches:	94
Percent Similarity:	44.1%	Conservative:	56
Best Local Similarity:	27.6%	Mismatches:	119
Query Match:	18.1%	Indels:	71
DB:	3	Gaps:	11

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US-10-041-018-22 (1-335) x US-09-692-570-1 (1-1664976)
QY 4 LysileAspGlu-----LeuileAsnAspProValTrpSerSerGlnAsn 19
Db 688576 AAAATTGATGAAGAAATTAAGACTTATGATGAGATAAGAT----- 688614
QY 20 GluSerLeuileSerIysProTyrAsn-----HisileLeuLeuIysProGlyIys 36
Db 688615 -----GATAAACATATATAACGCGTCAAAACATCTTCTATTGCTGGAGGAAG 688662
QY 37 AsnPheArgLeuAsnLeuValGlnIleAsnArgValMetAsnLeuProIysAspGln 56
Db 688663 AGAATTAGCCCATATTTAACTAGTA-----ACTTATATGTTGAAGAAAGCAT 688713
QY 57 LeuAlaIleVal-----SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeu 73
Db 688714 ATTGAGGAGGTTTGGCCAGCGCTGCTGCAGTAGAGTTAATTACAACTACACCTTAATA 688773
QY 74 IleAspAspileGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHisLeuIle 93
Db 688774 CATGATGACATTTATGACCAATGATGATGAGAGAGAGAGAAACCAACAGTTCATGTTGTC 688833
QY 94 PheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeu 113
Db 688834 TATGGAGAGCCCAATGGCTATCTTAGCTGGAGATTTATATATATGCTTAAAGCTTTTGAAGCA 688893
QY 114 ValSerGlnLeuThrThrIysGluProLeuTyrHisAsnLeuIleThrIlePheAsnGlu 133
Db 688894 GTTTCAGAATAAAGATAATAAAGAGCT---CATGAAGTTTAAATAATCCTATCAAAA 688950
QY 134 GluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspileTyrTrpArgAspPheLeuPro 153
Db 688951 GCATGTGTTCAGGTTTGTGAAGGCGCAGGCAATGGACATGGAATTTGAAAACACTAC----- 689004
QY 154 GluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnIysThrGlyGlyLeu 173
Db 689005 -----TATCCTACAAATGGAAGAAATCTTAGATATATGATAGAAAAGACAGAGCTTTA 689058
QY 174 PheArgLeuThrLeuArgLeuMetGluAlaLeuSerPro---SerSerHisGlyHis 192
Db 689059 TTAGAGGCTTCTGTGGGAATTTGGGCTGTTATGGCTGATTGTAATGAAGAAGAAAGGAA 689118
QY 193 SerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeu 212
Db 689119 GCATTAAGAGAGATATGCAAAAAGAAATGGATTAACTTTTCAAAATACAGGATGATGTTTA 689178
QY 213 AsnLeuIysAspPheGlnMetSerSerGluIysGlyPheAlaGluAspileThrGluGly 232
Db 689179 GATTTTAATTTGGGACACAGAAAAGTTAGTAAGCCAGTTGGGAAGTGATATAGAGAAGGT 689238
QY 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrIysThrIysGlyGlnThrGlu 252
Db 689239 AAAAGACAAATAATTGTTATCCAGCC----- 689265
QY 253 GlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspIysAspileIysLeu 272
Db 689266 -----CTAAAACAACTTGATGCAAGATAAAGAAA 689295
QY 273 LysLeuIleGlnIleLeu----- 278
Db 689296 AGATTATTGGAATTTTAGGAATAAATAATGTTAAGGATGAAGAAATTAAGAGCAAT 689355
QY 279 GluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMet 298
Db 689356 GAGATATTAAAGCCTTCAATTGATATGCAAAAGAACTTATGAAACAAAACCTGAAGAA 689415
QY 299 IleLys-----AsnAspAsnGluAsnIysTyrIleArgAspAspTyrLeuAla 312
Db 689416 GCAAAAGAAATATTAAAGATATTCAATATAAGACAGAAGGAAAGTTTATAGAGGATTTGGCT 689475
RESULT 9
US-09-543-681A-1736
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; Sequence 1736, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1736
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1736

Alignment Scores:
Pred. No.: 4,99e-19 Length: 924
Score: 242.50 Matches: 77
Percent Similarity: 47.2% Conservative: 67
Best Local Similarity: 25.2% Mismatches: 132
Query Match: 14.1% Indels: 29
DB: 3 Gaps: 8

US-10-041-018-22 (1-335) x US-09-543-681A-1736 (1-924)
QY 4 LysileAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGluSerLeuIle 23
Db 61 CQTGTTGATGAAGCACTCAACCAAGCGCTACAAACGTTGCGCTTTTCTGATATGCCACTC 120
QY 24 SerLysProTyrAsnHisIleLeuLeuIysProGlyIysAsnPheArgLeuAsnLeuIle 43
Db 121 AGCCAAAGCAATCGCTACGAGCACTCTTTGGGGGGGAAACGTTTACGCCCATTTCTCGTT 180
QY 44 ValGlnIleAsnArgValMetAsnLeuProIysAspGlnLeuAlaIleValSerGlnIle 63
Db 181 TATGGGTTAGGAGAATGTTTAACTGTTGCTGTTGCTAATCTTGATGTGCCAGCGCGCT 240
QY 64 ValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspileGlu-----AspAsnAla 81
Db 241 ATTGATGTATTTCATGTCATATTCCTACCTGATCCATCAGCACTTACCTGCAATGGACAATGAT 300
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
Db 301 GATTTACGTCGAGGAAACCCACTTGTCTATATTTAGTTTGGCGAAGCCCAATGCCATTTTA 360
QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
Db 361 GCGGGTGTGCAATTACAAACCTTTGGCCTTTGAAATTTTAGCCCAAAATGCGATGCTGAT 420
QY 122 ProLeuTyrHisAsnLeuIleThrIlePheAsnGlu-----GluLeuIle 136
Db 421 CTCGCCATTGGCCGATCGCGTAGCCATGATTGCTGAATTAGCCACCAAGTGGTTTAGCG 480
QY 137 AsnLeuHisArgGlyGlnGlyLeuAspileTyrTrpArgAspPheLeuProGluIleIle 156
Db 481 GGTATGTGTGTGTCGACAGGCACCTTGATCTTGTATGTCGCGAAGATAAAATCAATGTATCTGTC 540
QY 157 ProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeu 176
Db 541 GCTCTTGAGAAATAATTCATTTA-----CATAAAACAGCTGCGTTAATTCGTGCA 588
QY 177 ThrLeuArgLeuMetGluAlaLeuSerProSerHisGlyHisSerLeuValPro 196
Db 589 GCGGTTTCGCTA---GGGCGCACTAGC---GCAGGGCAAAAGGCGACCATGTGTTACCT 642
QY 197 -----PheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeu 212
Db 643 GCACCTGGATAAATATATCCCACTCTATAGGCTTTCAGTTTCCAAAGTTCCAGGATGATTTTA 702
QY 213 AsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspileThrGluGly 232
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Db 703 GATGTTATTGGGACACTGAAGAGACTGGAAAGCGACAGGGAAGTGATCAAGAAGCTGGA 762
Qy 233 LysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGlu 252
Db 763 AAAAGTACTTATCCGGCTCTACTTGGTTAGCACAAGCACAAGAAAGACACAG--GAA 819
Qy 253 GlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeu 272
Db 820 TTGTATAACGAAGCATTTGGAT-----GCCTTA 846
Qy 273 LysLeuIleGlnLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIle 292
Db 847 GCCTTCTTGAACAATACGAGTACGATACCTCTACGCTAAACAATTAAGCGAATTTATC 906
Qy 293 AsnGlnLeuValAsn 297
Db 907 GTAGAACGGGAAAC 921

RESULT 10

US-08-705-377-4
; Sequence 4, Application US/08705377
; Patent No. 5807725
; GENERAL INFORMATION:
; APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
; APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
; TITLE OF INVENTION: Long-Chain Prenyl Diphosphate Synthase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,377
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7247043
; FILING DATE: 01 SEP 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/442

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993
; TYPE: Nucleic acid
; STRANDEDNESS: Double strand
; TOPOLOGY: Linear

MOLECULE TYPE: Mutated genomic DNA
US-08-705-377-4

Alignment Scores:
Pred. No.: 4,99e-18 Length: 993
Score: 234.50 Matches: 84
Percent Similarity: 46.3% Conservative: 65
Best Local Similarity: 26.1% Mismatches: 150
Query Match: 13.6% Indels: 23
DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-08-705-377-4 (1-993)
; Sequence 4, Application US/09052962
; Patent No. 5882909
; GENERAL INFORMATION:

Qy 6 AspGluLeuIleAsnAsn---AspProValTrpSerSerGlnAsnGluSerLeuIleSer 24
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Qy 25 LysProTyrAsn-----HisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
Db 85 AAATATATGAAGCCTCATATCATCTCTGAGGTAAGAGGTTAAGACCATTA 144
Qy 42 LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
Db 145 ATCTTAACATATATCATCAGATTATTTCGGAGGACAGAGAAAGAGCTTATTATGCGAGT 204
Qy 62 GlnIleValGlnLeuLeuIleAsnSerSerLeuLeuIleAspAspIleGluAspAsnAla 81
Db 205 GCAGCTATTGAAGTCTTCTCATCTTCTACGCTTGTGCATGATATATATGATCAAGAT 264
Qy 82 ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
Db 265 AATATCAGAAGAGGGTTACCCACAGTCCACGTGAATATACGCTTACCTTTAGCAATATTA 324
Qy 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
Db 325 GCTGGGGATTACTACATGCAAGGCTTTTACGCTTTAAACCCAGGCTCTTAGAGGTTTG 384
Qy 122 Pro-----LeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHis 139
Db 385 CCAAGTGAAACCATTAATTAAGGCTTTTCGATATTTTCACTCGTTCAATAATAATATATCC 444
Qy 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGln 159
Db 445 GAAGCAGCAGCAGTAGATATGAATTTGAGGACAGAAATTCAT-----ATAAAGGAGCAG 498
Qy 160 GluMetTyrIleuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
Db 499 GAA---TACCTTGACATGATCTCACGTAAGCAGCTGCATTTATCTCGGCATCTCCTCAAGT 555
Qy 180 LeuMetGluAlaLeuSerProSerHisHisGlyHisSerLeuVal---ProPheIle 198
Db 556 ATAGGCGCCTTATGCTGGTGTCTAATGATGATGATGATGATGATGATGATGATGATGATG 615
Qy 199 AsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGln 218
Db 616 ACGAATCTAGTATTGCAATTCAGATTGTTGACGATATCTTAGGTCTTAACAGCAGACGAA 675
Qy 219 MetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIle 238
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Qy 239 ValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeu 258
Db 736 ATAAACACTGGAGCTTTGTAAA-----GAGGACGAGAGAGAGATGTCCTA 783
Qy 259 ArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuGlnIleLeu 278
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Qy 279 GluPheAspThrAsnSerLeuAlaTyrThr-----LysAsnPheIle 292
Db 844 AAGAAATATCTCTTTTAGATTATGATACAAATTTAGCAGAGAAATATATATAAAATGCTATA 903
Qy 293 AsnGlnLeuValAsnMetIle-----LysAsnAspAsnGluAsnLysTyrLeuProAsp 310
Db 904 GACTCTTTA---AATCAAGTCTCTCTAGAGGTATATACCTCGAAGAGGCTTTAAATAT 960
Qy 311 LeuAla 312
Db 961 CTAGCT 966

RESULT 11

US-09-052-962-4
; Sequence 4, Application US/09052962
; Patent No. 5882909
; GENERAL INFORMATION:

APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
TITLE OF INVENTION: Nucleic Acid Encoding Mutant
TITLE OF INVENTION: Geranylgeranyl Diphosphate Synthase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,962
FILING DATE: Concurrent Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,377
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: JP 7247043
FILING DATE: 01 SEP 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 77670/545
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993
TYPE: Nucleic acid
STRANDEDNESS: Double strand
TOPOLOGY: Linear
MOLECULE TYPE: Mutated genomic DNA
US-09-052-962-4

Alignment Scores:
Pred. No.: 4,99e-18 Length: 993
Score: 234.50 Matches: 84
Percent Similarity: 46.3% Conservative: 65
Best Local Similarity: 26.1% Mismatches: 150
Query Match: 13.6% Indels: 23
DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-09-052-962-4 (1-993)

QY 6 AspGluLeuLeuAsnAsn---AspProValTyrSerSerGlnAsnGluSerLeuIleSer 24
Db 25 AATGAGATTGTTAACTCTTAACGACATATTAAGAGCTATATCTCGAGATGTTCT 84
QY 25 LysProTyrAsn-----HisLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
Db 85 AAACCTATGAAGCCCTCATATCTTTTACATCTGGAGGTTAAGAGCCATTA 144
QY 42 LeuIleValGlnLeuAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
Db 145 ATCTTAACATATATCATCATGATTTCGAGGACAGAGAAAGAGCTTATTATGCAGT 204
QY 62 GlnIleValGluLeuLeuHisAsnSerSerLeuLeuLeuAspIleGluAsnAla 81
Db 205 GCAGCTATTGAGTCTTCTTACTTCTACGCTTGTCATGATGATATATGATCAAGAT 264
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
Db 265 AATATCAGAAGAGGGTTACCCACAGCCACGTCAGGTAATACGGCTTACCTTAGCAATATTA 324
QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121

Db 325 GCTGGGAATTACTACATGCAAGGCTTTTACGCTCTTAACCCAGGCTCTTAGAGGTTTG 384
QY 122 Pro-----LeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuAsnLeuHis 139
Db 385 CCAAGTGAAACCAATAATTAAGGCTTTTCGATATTTTCACTCGTTCAATAATAATTATATCC 444
QY 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleLeuProThrGln 159
Db 445 GAAGGACAGGCGATAGATATGGAATTTGAGGACAGAAATTGAT-----ATAAGGAGCAG 498
QY 160 GluMetTyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArg 179
Db 499 GAA---TACCTTGACATGATCTCAGTAGACAGCGCTGCATTTATTCGCGCATCTCAAGT 555
QY 180 LeuMetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuVal---ProPheIle 198
Db 556 ATAGGCGCACTTATTGCTGGTCTAATGATATAATGATGTAAGACTGATGCTCGATTTCGGT 615
QY 199 AsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGln 218
Db 616 ACGAATCTAGGTATTGCAATTTTCAGATTGTTGACGATATCTTAGGCTTAACAGCAGCGAA 675
QY 219 MetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIle 238
Db 676 AAGGAACCTTGGAAAGCCTGTTTTTGTAGTATATTAGGAGGGTAAAGAGACTATATCTGTA 735
QY 239 ValHisAlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluLeu 258
Db 736 ATAAAAACACACTGGAGCTTTGTAAA-----GAGGACGAGAGAAGATTGTCCTA 783
QY 259 ArgIleLeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeu 278
Db 784 AAGGCGTTAGGTAAATAAGTCAGCCTCAAAGAAGAAATTAATGAGCTCAGCAGATATAAT 843
QY 279 GluPheAspThrAsnSerLeuAlaTyrThr-----LysAsnPheIle 292
Db 844 AAGAAATCTCTTTAGATTATGATACATATTTAGCAGAGAAATATTTATAAATATGCTATA 903
QY 293 AsnGlnLeuValAsnMetIle-----LysAsnAspAsnGluAsnLysTyrLeuProAsp 310
Db 904 GACTCTTTA---AATCAAGTCTCTCTTAAGAGTGATATACCTGGAAAGGCTTTAAAAATAT 960
RESULT 12
US-09-053-068-4
Sequence 4, Application US/09053068
Patent No. 5885810
GENERAL INFORMATION:
APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
TITLE OF INVENTION: Process for The Production of Prenyl
TITLE OF INVENTION: Diphosphate and Mutants Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,068
FILING DATE: Concurrent Herewith
CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,377
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: JP 7247043
; FILING DATE: 01 SEP 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993
; TYPE: Nucleic acid
; STRANDEDNESS: Double strand
; TOPOLOGY: Linear
; MOLECULE TYPE: Mutated genomic DNA
; US-09-053-068-4

Alignment Scores:
Pred. No.: 4.99e-18 Length: 993
Score: 234.50 Matches: 84
Percent Similarity: 46.3% Conservative: 65
Best Local Similarity: 26.1% Mismatches: 150
Query Match: 13.6% Indels: 23
DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-09-053-068-4 (1-993)

QY 6 AspGluLeuLeuAsnAen---AppProValTrpSerSerGlnAenGluSerLeuLeuSer 24
DB 25 AATGAGATTGTAATTCGTAAACGACATTAATTAAGAGCTATATATCTGGAGATGTTCT 84
QY 25 LysProTyrAsn-----HisLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
DB 85 AAATATATGAGCTCATATCATTTCTTTACATCTCGAGGTAAGAGTTAAGACCATTA 144
QY 42 LeuLeuValGlnLeuAenArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
DB 145 ATCTTAATCATATCATCATGATTATTTCGGAGGACAGAGAAAGAGCTTATTATGCAGGT 204
QY 62 GlnIleValGluLeuLeuHisAenSerSerLeuLeuLeuAspAspIleGluAspAenAla 81
DB 205 GCAGCTATTGAGTCTTCACTTCTTACCTGTGTCATGATGATATATGATGATCAAGAT 264
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
DB 265 AATATCAGAAGAGGGTTACCCACAGTCCAGTGAATACGGCTTACCCTTAGCAATATTA 324
QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
DB 325 GCTGGGGATTACTACATGCAAGGGCTTTTCAGCTCTTAACCCAGGCTCTTAGAGGTTTG 384
QY 122 Pro-----LeuTyrHisAenLeuLeuThrIlePheAsnGluGluLeuLeuHis 139
DB 385 CCAAGTGAACCAATAATTAAGGCTTTCGATATTTCATCGTTCAATAATAATATATATCC 444
QY 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluLeuIleProThrGln 159
DB 445 GAAGGACAGGACGATAGATGGAATTGAGACAGATTCAT-----ATAAGGAGCAG 498
QY 160 GluMetTyrLeuAenMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArg 179
DB 499 GAA---TACCTTGACATGATCTCACGTAAGACAGCTGCATTTATTTCTCGGCATCTCAAGT 555
QY 180 LeuMetGluAlaLeuSerProSerSerHisGlyHisSerLeuVal---ProPheIle 198
DB 556 ATAGGCGGCATTTATGCTGTGTGTAATGATAATGATGATGATGATGATGATGATGATGAT 615
QY 199 AsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGln 218

DB 616 ACGAATCTAGGTATTGCAATTTTCAGATTGTTGACGATATCTTAGGTCTTAACAGCAGACGAA 675
QY 219 MetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIle 238
DB 676 AAGGAACCTTGGAAAGCCTGTTTATGATATATTAGGAGGGTAAAGACATATATCTGTA 735
QY 239 ValHisAlaLeuAenPheThrLysThrLysGlyGlnThrGluGlnHisAenGluIleLeu 258
DB 736 ATAAACACACTGGAGCTTTTGTAAA-----GAGGACGAGAAGAAGATTGTCCTA 783
QY 259 ArgIleLeuLeuAenArgThrSerAspLysAspIleLysLysLeuIleGlnIleLeu 278
DB 784 AAGCGTGTAGGTAATAAGTCAGCTCAAAAGAAGAATTAATGAGCTCAGCAGATATAAT 843
QY 279 GluPheAspThrAenSerLeuAlaTyrThr-----LysAenPheIle 292
DB 844 AAGAAATACCTTTTAGATTATGATACAAATTTAGCAGAGAAATATTATAAAATGCTATA 903
QY 293 AsnGlnLeuValAsnMetIle-----LysAenAspAenGluAenLysTyrLeuProAsp 310
DB 904 GACTCTTTA---AATCAAGTCTCTCTAAGAGTGATATACCTGGAAAGGCTTTAAATAT 960
QY 311 LeuAla 312
DB 961 CTAGCT 966
RESULT 13
US-09-252-991A-4877
; Sequence 4877, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4877
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4877
Alignment Scores:
Pred. No.: 7.92e-18 Length: 1026
Score: 233.00 Matches: 65
Percent Similarity: 48.2% Conservative: 81
Best Local Similarity: 21.5% Mismatches: 135
Query Match: 13.5% Indels: 22
DB: 3 Gaps: 6
US-10-041-018-22 (1-335) x US-09-252-991A-4877 (1-1026)
QY 22 LeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
DB 148 CTGGTGGAAAAGATCGCGAGCTACATCATCTCCGCGGGCGCAAGCGCTCGCGCCGCTG 207
QY 42 LeuIleValGlnLeuAenArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
DB 208 CTGGTCTCTGCTCGCGGCAAGACCTTGGGCTACAGGGCGACGACCTCTGCTGCTGCC 267
QY 62 GlnIleValGluLeuLeuHisAenSerSerLeuLeuLeuAspAspIleGluAsnAla 81
DB 268 GCCACCATCGAATTCCTGACACCTCACTCTCTGACAGCAGCTGTCGAGCCCTCC 327
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
DB 328 GGCTCGCGCGCGCGCTCCACCGCAATGCTCTGCGGCAAGCGCGCGCGCGCTGCTG 387

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QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
Db 388 GTAGGCGACTTCTTTATCGCGCTCTTCGAAATGATGTCGAGCTGGTTCATCGCG 447
QY 122 ProLeuTyrHisAsnLeuThrLeuPheAsnGluGluLeuLeuAsnLeuHisArgGly 141
Db 448 -----GTCATGGCATCATATCCAGCCACCGCGGTGATCGCCGAGGCG 492
QY 142 GlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleLeuProThrGlnGluMet 161
Db 493 GAAGTGCTCAATG-----TCCAAGTACGCGACGCCAGCACTACCGAGAGACC 543
QY 162 TyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeuMet 181
Db 544 TACATGGAAGTGTCCGCGCGCAAGACGCGATGCTTTTCGAGCGCTTCGACCCACACGCGCC 603
QY 182 GluAlaLeu--SerProSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
Db 604 GCGCGCTGTCCAGCGCGGAGGAGACAGTCCGAGGCACTGCGCGCTTCGCGGACTAC 663
QY 201 LeuGlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 664 CTGGGAATCGCTTCAGCTGTGGAGACGACTCTCGACTACCGCGCGGACCGCGGACC 723
QY 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 724 CTCGGCAAGACGTCCGCGGACGACCTTCGCGGAGGCAAGCCACCTACCGCTGTATCGTC 783
QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluLeuArgIle 260
Db 784 ACATG-----CGTAGCGGACCGGAGGAGCGCGCTGTGTACGCAAG 828
QY 261 LeuLeuLeuArgThrSerAspLysAspIleLys-----LeuLysLeuIle 275
Db 829 GCCATCCAGACGGCGGACCGGACGACTGTGGAGAGCGTGTGTCCCGCTCGAGGCTGCC 888
QY 276 GlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeu 295
Db 889 GCGCGCTCGGATATACCGCCCAAC-----CTCGCGCGGACCTACCGCGCGCGCGCC 939
QY 296 ValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSer 315
Db 940 ATCGCTCGCTGATACGCTGCGGACACGAATACCGCTCGCGCGCTGTGTAACCTCAGC 999
QY 316 AspThrAla 318
Db 1000 GAATTCGCT 1008

RESULT 14
US-09-248-796A-3882
; Sequence 3882, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3882
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3882
Alignment Scores: 3.39e-18 Length: 498
Pred. No.:

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Score: 232.00 Matches: 67
Percent Similarity: 53.3% Conservative: 30
Best Local Similarity: 36.8% Mismatches: 57
Query Match: 13.5% Indels: 28
DB: 3 Gaps: 8

US-10-041-018-22 (1-335) x US-09-248-796A-3882 (1-498)

QY 162 TyrLeuAsnMetValMetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeuMet 181
Db 10 TATTTGGAAATGATTAAAGATAAACTGGTGGTTCAGATTGGCAATCAAAATTATG 69
QY 182 GluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheIleAsnLeu 201
Db 70 CTGTTGTATTTCAGATGTACAGAAAC---GATCAATTAATATCCCTTCGCAAAATTAATG 126
QY 202 GlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSerSer 221
Db 127 GGCATTTTGTATCAAGTTAGACGCGATTAATTTGAATTTAGTGATGCCAAGTATTCTCGC 186
QY 222 GluLysGly---PheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 187 ATGAAAGGCACATACATGTGAGACTTGATAGAGGAAAGTATCATTTGCTATATACAT 246
QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluLeuArgIle 260
Db 247 TGTCTAAGAACCACTAAG-----GATTCACCTGTACACAAATA 285
QY 261 LeuLeuLeuArgThrSerAspLysAsp-----IleLysLeuLys 273
Db 286 CTATATGATTACGACTCTAGCTCCGATCGTGTTCCTCAAAATCTTTAATTCATTAACT 345
QY 274 LeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsn 293
Db 346 TTA---AGCTTTATGAAATAAGTCCAAATCTTTGGAGTATACATGAATTAATTAAG 402
QY 294 GlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSer 313
Db 403 GTATTGGAAAGAAATTAAGA---CAATGATTTTGAAGTAT---CCTGAGCTGGAGAAC 456
QY 314 HisSerAspThrAlaThrAsnLeuHisAspGluLeuLysTyrIleIleAspHisLeuSer 333
Db 457 TCTGCA-----TTATTCAAAATTTCTTGACCGTTTATGT 489
QY 334 GluLeu 335
Db 490 GATCTT 495

RESULT 15
US-08-705-377-3
; Sequence 3, Application US/08705377
; Patent No. 5807725
; GENERAL INFORMATION:
; APPLICANT: OHTO, Chikara, ASADA, Chika, OHNUMA, Shinichi,
; APPLICANT: NISHINO, Tokuzo, HIROOKA, Kazutake, HEMMI, Hisashi
; TITLE OF INVENTION: Long-Chain Prenyl Diphosphate Synthase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,377
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 435

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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7247043
; FILING DATE: 01 SEP 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toiffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-429-1776
; TELEFAX: 202-429-0796
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993
; TYPE: Nucleic acid
; STRANDEDNESS: Double strand
; TOPOLOGY: Linear
; MOLECULE TYPE: Mutated genomic DNA
US-08-705-377-3

Alignment Scores:
Pred. No.: 1.49e-17 Length: 993
Score: 230.50 Matches: 83
Percent Similarity: 46.3% Conservative: 66
Best Local Similarity: 25.8% Mismatches: 150
Query Match: 13.4% Indels: 23
DB: 2 Gaps: 10

US-10-041-018-22 (1-335) x US-08-705-377-3 (1-993)

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Qy 6 AspGluLeuLeuAanAan---AspProValTrpSerSerGlnAanGluSerLeuLeuSer 24
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 AATGAGATTGTTAATCTGTAAACGACATTATTAAAGAGCTATATATCTGGAGATGTTTCT 84
Qy 25 LysProTyrAan-----HisIleuLeuLysProGlyLysAanPheArgLeuAan 41
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
85 AAACATATGAAGCCTCATATCATTTCTGTACATCTGGAGGTAAAGACCAATTA 144
Qy 42 LeuIleValGlnIleAanArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
145 ATCTTAACATATATCATGATTATTTCGGAGGACAGAGAAAGAGCTTATTATGACAGGT 204
Qy 62 GlnIleValGluLeuLeuHisAsnSerSerLeuLeuLeuAspIleGluAspAanAla 81
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
205 GCAGCTATTGAGTTCTTCATCTTTACGCTTGTGCATGATGATATATGATCAAGAT 264
Qy 82 ProLeuArgArgGlyGlnThrThrSerHisLeuLeuPheGlyValProSerThrIleAan 101
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
265 AATATCAGAGAGGGTTACCCACAGTCACGTCGAATACGGCTTACCCTTAGCAATATTA 324
Qy 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGlu 121
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
325 GCTGGGATTACTACATGCAAGGCTTTCAGCTCTTAACCCAGGCTCTTAGAGGTTTG 384
Qy 122 Pro-----LeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuLeuAsnLeuHis 139
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
385 CCAAGTGAACCAATAATTAAGCTTTTCGATATTTTCACTCGTCAATAATAATTATATCC 444
Qy 140 ArgGlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGln 159
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
445 GAAGGACAGGCGATGATGGAATTTTGAGGACAGAATTGAT-----ATAAAGGAGCAG 498
Qy 160 GluMetTyrLeuAanMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArg 179
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
499 GAA---TACCTTGACATGATCTCACGTAAGACAGCTGCATTTATTCTCGGCATCCTCAAGT 555
Qy 180 LeuMetGluAlaLeuSerProSerHisHisGlyHisSerLeuVal---ProPheIle 198
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
556 ATAGCGCATTATTGCTGGTCTAATGATGAATGATGAAGACTGATGCTGATTCGGT 615
Qy 199 AsnLeuLeuGlyIleIleTyrGlnIleArgAspAspTyrLeuAanLeuLysAspPheGln 218
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 ACGAATCTAGGATTGCAATTTCAGATTGTTGACCATATCTTAGGTCTTAACAGCAGACGAA 675
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Qy 219 MetSerSerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIle 238
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
676 AAGGAACCTTGGAAAGCCTGTTTATTAGTGATATTAGGAGGGTAAAGAGACTATATCTGTA 735
Qy 239 ValHisAlaLeuAanPheThrLysGlyGlnThrGluGlnHisAanGluIleLeu 258
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
736 ATAAAAACACTGGAGCTTTGTAAA-----GAGGACGAGAGAAGAGATTGTCTCTA 783
Qy 259 ArgIleLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeu 278
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
784 AAGCGTTAGGTAAATAGTCAGCCTCAAAAGAAGAAATTAATAGCTCAGCAGATATAATT 843
Qy 279 GluPheAspThrAanSerLeuAlaTyrThr-----LysAsnPheIle 292
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
844 AAGAAATACCTCTTTAGATTATGATCAATTTAGCAGAGAAATATTATAAAATGCTATA 903
Qy 293 AsnGlnLeuValAanMetIle-----LysAsnAspAanGluAanLysTyrLeuProAsp 310
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
904 GACTCTTTA---AATCAAGTCTCTCTAAGAGTGATATACCTCGAAAGGCTTTAAATAT 960
Qy 311 LeuAla 312
Db :|||:|||||
961 CTAGCT 966
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Job time : 721.758 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2006, 07:57:49 ; Search time 726.582 Seconds
(without alignments)
3812.705 Million cell updates/sec

Title: US-10-041-018-22

Perfect score: 1720

Sequence: 1 MEAKIDELINNDPVSSQNE.....DTATNLHDELLYIDHLSL 335

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 segs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=200000000 -HOST=abes04

-USER=US10041018 @CGN 1.1.1364 @runat_14022006_080436_25112 -NCPU=6 -ICPU=3

-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:

4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:

7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:

8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1720	100.0	1008	6	US-10-369-493-46181
2	1720	100.0	1008	7	US-10-450-941-5
3	1720	100.0	1563	7	US-10-041-018-1
4	974	56.6	599	9	US-10-487-901-363
5	629.5	36.6	1044	6	US-10-369-493-36092
6	623	36.2	1284	6	US-10-369-493-27908
7	584	34.0	1395	6	US-10-189-268-4

8	584	34.0	1692	3	US-09-814-353-21762	Sequence 21762, A
9	584	34.0	2534	7	US-10-041-018-3	Sequence 3, Appli
10	577	33.5	2529	3	US-09-925-302-171	Sequence 171, App
11	577	33.5	2529	3	US-09-925-302-171	Sequence 171, App
12	545.5	31.7	2210	10	US-11-097-143-9632	Sequence 9632, Ap
13	545.5	31.7	2222	7	US-10-041-018-21	Sequence 21, Appl
14	541.5	31.5	1364	6	US-10-369-493-36669	Sequence 36669, A
15	538	31.3	1882	7	US-10-001-192A-14	Sequence 14, Appl
16	537.5	31.2	1888	8	US-10-357-930-25125	Sequence 25125, A
17	525.5	30.6	51001	6	US-10-189-268-11	Sequence 11, Appl
18	488.5	28.4	1843	7	US-10-041-018-5	Sequence 5, Appli
19	475.5	27.6	961	6	US-10-369-493-36678	Sequence 36678, A
20	395	23.0	716	3	US-09-969-034-1924	Sequence 1924, Ap
21	380	22.1	912	6	US-10-369-493-36606	Sequence 36606, A
22	374.5	21.8	7837	7	US-10-041-018-2	Sequence 2, Appli
23	370	21.5	6977	10	US-11-097-143-9631	Sequence 9631, Ap
24	357.5	20.8	935	6	US-10-369-493-36350	Sequence 36350, A
25	337	19.6	1044	7	US-10-282-122A-10905	Sequence 10905, A
26	310.5	18.1	984	6	US-10-369-493-45179	Sequence 45179, A
27	305.5	17.8	554	3	US-09-969-034-1324	Sequence 1324, Ap
28	290.5	16.9	593	3	US-09-969-034-1488	Sequence 1488, Ap
29	278.5	16.2	1095	7	US-10-282-122A-40388	Sequence 40388, A
30	246.5	14.3	966	7	US-10-282-122A-32007	Sequence 32007, A
31	243.5	14.2	972	7	US-10-282-122A-42025	Sequence 42025, A
32	242.5	14.1	921	7	US-10-282-122A-32509	Sequence 32509, A
33	239	13.9	978	6	US-10-369-493-24788	Sequence 24788, A
34	238.5	13.9	975	7	US-10-282-122A-29902	Sequence 29902, A
35	238.5	13.9	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
36	236	13.7	972	7	US-10-282-122A-29211	Sequence 29211, A
37	234	13.6	966	6	US-10-369-493-37633	Sequence 37633, A
38	233	13.5	969	3	US-09-815-242-7933	Sequence 7933, Ap
39	233	13.5	969	7	US-10-282-122A-30502	Sequence 30502, A
40	228.5	13.3	966	7	US-10-282-122A-33315	Sequence 33315, A
41	227	13.2	963	7	US-10-282-122A-15089	Sequence 15089, A
42	226.5	13.2	930	6	US-10-369-493-43383	Sequence 43383, A
43	226	13.1	972	7	US-09-815-242-9636	Sequence 9636, Ap
44	226	13.1	972	7	US-10-282-122A-38868	Sequence 38868, A
45	226	13.1	972	7	US-10-282-122A-39465	Sequence 39465, A

ALIGNMENTS

RESULT 1

US-10-369-493-46181

; Sequence 46181, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369, 493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 46181

; LENGTH: 1008

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

; US-10-369-493-46181

Alignment Scores:

Pred. No.: 3 58e-181

Score: 1720.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 6

Length: 1008

Matches: 335

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

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QY 1 MetGluAlaLysIleAspGluLeuIleAsnAsnAspProValTrpSerGlnAsnGlu 20
Db 1 ATGGAGCCCAAGATAGATGAGCTGATCAATATGATCCTGTTGGTCCAGCCAAATGAA 60
QY 21 SerLeuIleSerIysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 61 AGCTTGATTTCAAAACCTTATAATCACAATCCTTTGAAACCTGGCAAGAACTTTAGACTA 120
QY 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 121 AATTTAATAGTTCAAAATTAACAGAGTTATGAAATTTGCCCAAAGACCAGCTGGCCATAGT 180
QY 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn 80
Db 181 TCGCAAAATTTGAGCTCTTGCAATAATTCAGCCCTTTAATCGAGATATAGAGATAAT 240
QY 81 AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
Db 241 GCTCCCTTGAGAAGGGGACAGACCACTTCTCAATCTCGGTGTACCTCCACTATA 300
QY 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrLys 120
Db 301 AACCCGCAAAATTAATATGTTATTCAGAGCCATGCAACTTGTATCGCAGCTAACCCAA 360
QY 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
Db 361 GAGCCTTTGTATCATAAATTTGATTAGATTTTCACAGAAAGATTCATCAATCTACATAGG 420
QY 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
Db 421 GGACAAGGCTTGATATATCTAGTGGAGAGACTTTCTGCCTGAAATCATACTACTCAGGAG 480
QY 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
Db 481 ATGTATTTGAATATGTTATGTAATAAACAAGCGGCTTTTCAGATTAACGTGAGACTC 540
QY 181 MetGluAlaLeuSerProSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
Db 541 ATGGAAAGCGCTGTCCTCTCCACACACAGGCCATTCGTTGGTTCCTTTTATAAATCTT 600
QY 201 LeuGlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 601 CTGGGTATTTATTTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTCCAAATGTCC 660
QY 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 661 AGCGAAAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 720
QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
Db 721 GCCCTTAACCTTCACTAAACAGAAAGGTCAAACTGAGCAACACAAATGAAATTTCTAAGAA 780
QY 261 LeuLeuLeuArgThrSerAspIysAspIleLysLeuLysLeuIleGlnIleLeuGluPhe 280
Db 781 CTCCTGTTGAGGACAAGTGATAAGATATAAAACTAAAGCTGATTCAAAATACTGGAAATTC 840
QY 281 AspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 841 GACACCAATTCATTTGGCCCTACACCAAAAAATTTTATTAATCAATAGTGAATATGATAAAA 900
QY 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 901 AATGATAATGAAAATPAAGTATTTTACCTGATTTGGCTTCGCAATCCGACACCGCCACCA 960
QY 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 961 TTACATGACGAATTTGTTATATATATATATAGACCACCTTATCCGAATTG 1005
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RESULT 2

US-10-450-941-5

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; Sequence 5, Application US/10450941
; Publication No. US20040063182A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: A METHOD OF PRODUCING PRENYLALCOHOL
; FILE REFERENCE: PH-1444PCT
; CURRENT APPLICATION NUMBER: US/10/450,941
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: JP2000-401701
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP2000-403067
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP2001-282978
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1005)
; US-10-450-941-5

Alignment Scores:
Pred. No.: 3,58e-181 Length: 1008
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

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Db 1 ATGGAGCCCAAGATAGATGAGCTGATCAATATGATCCTGTTGGTCCAGCCAAATGAA 60
QY 21 SerLeuIleSerIysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 61 AGCTTGATTTCAAAACCTTATAATCACAATCCTTTGAAACCTGGCAAGAACTTTAGACTA 120
QY 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 121 AATTTAATAGTTCAAAATTAACAGAGTTATGAAATTTGCCCAAAGACCAGCTGGCCATAGT 180
QY 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn 80
Db 181 TCGCAAAATTTGAGCTCTTGCAATAATTCAGCCCTTTAATCGAGATATAGAGATAAT 240
QY 81 AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
Db 241 GCTCCCTTGAGAAGGGGACAGACCACTTCTCAATCTCGGTGTACCTCCACTATA 300
QY 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrLys 120
Db 301 AACCCGCAAAATTAATATGTTATTCAGAGCCATGCAACTTGTATCGCAGCTAACCCAA 360
QY 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
Db 361 GAGCCTTTGTATCATAAATTTGATTAGATTTTCACAGAAAGATTCATCAATCTACATAGG 420
QY 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
Db 421 GGACAAGGCTTGATATATCTAGTGGAGAGACTTTCTGCCTGAAATCATACTACTCAGGAG 480
QY 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
Db 481 ATGTATTTGAATATGTTATGTAATAAACAAGCGGCTTTTCAGATTAACGTGAGACTC 540
QY 181 MetGluAlaLeuSerProSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
Db 541 ATGGAAAGCGCTGTCCTCTCCACACACAGGCCATTCGTTGGTTCCTTTTATAAATCTT 600
QY 201 LeuGlyIleIleTyrGlnIleArgAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 601 CTGGGTATTTATTTATCAGATTAGAGATGATTACTTGAATTTGAAAGATTTCCAAATGTCC 660
QY 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 661 AGCGAAAAAGGCTTTGCTGAGGACATTACAGAGGGGAAGTTATCTTTTCCCATCGTCCAC 720
QY 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
Db 721 GCCCTTAACCTTCACTAAACAGAAAGGTCAAACTGAGCAACACAAATGAAATTTCTAAGAA 780
QY 261 LeuLeuLeuArgThrSerAspIysAspIleLysLeuLysLeuIleGlnIleLeuGluPhe 280
Db 781 CTCCTGTTGAGGACAAGTGATAAGATATAAAACTAAAGCTGATTCAAAATACTGGAAATTC 840
QY 281 AspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 841 GACACCAATTCATTTGGCCCTACACCAAAAAATTTTATTAATCAATAGTGAATATGATAAAA 900
QY 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 901 AATGATAATGAAAATPAAGTATTTTACCTGATTTGGCTTCGCAATCCGACACCGCCACCA 960
QY 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 961 TTACATGACGAATTTGTTATATATATATATAGACCACCTTATCCGAATTG 1005
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Db 541 ATGGAAGCGTGCTCTCTCTCCACACCGCGCAATTCGTTGGTTCCTTTTCATAAATCTT 600
Qy 201 LeuGlyIleIleTyrGlnIleAArgAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 601 CTGGGTATATATATCATGATTAGATGATTTACTTGAATTTGAAGATTTCCAAATGTCC 660
Qy 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 661 AGCGAAAAGGCTTCTGCTGAGGACATTTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 720
Qy 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisGlnIleLeuArgIle 260
Db 721 GCCCTTTAACTTCACTAAACGAAAGGTCAAACTGAGCAACACCAATGAAATTTCTAAGAATT 780
Qy 261 LeuLeuLeuArgThrSerAspLysAspIleLeuLeuLysLeuIleGlnIleLeuGluPhe 280
Db 781 CTCTGTGTGAGGCAAGTGAAGATATAAATAAAGCTGATTTCAAAATCTGGAATTC 840
Qy 281 AspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 841 GACACCAATTCATTTGGCTACACCAAAAATTTTATTAATCAATAGTAGTGAATGATAAAA 900
Qy 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 901 AATGATAATGAAATAAGTATTTACCTGATTTGGCTTCGCATTCGACACCGCCCAAT 960
Qy 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 961 TTACATGACGAATTTGTATATATAATAGACCACTTATCCGAATTTG 1005

RESULT 3

US-10-041-018-1
; Sequence 1, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-041-018-1

Alignment Scores:

Pred. No.: 7.27e-181 Length: 1569
Score: 1720.00 Matches: 335
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-041-018-22 (1-335) x US-10-041-018-1 (1-1569)

Qy 1 MetGluAlaLysIleAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu 20
Db 301 ATGGAGGCCAAGATAGATGAGCTGATCAATATGATCCTGTTGGTCCAGCCAAATGAA 360
Qy 21 SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
Db 361 AGCTTGATTTCAAACCTTATATATACATCTCTTTGAAACCTGGCAAGAACTTTAGACTA 420
Qy 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
Db 421 AATTTAATAGTTCAATTAACAGATTATGAAATTTGCCCAAGACCGAGCTGGCCATAGTT 480

Qy 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn 80
Db 481 TCGCAAAATGTTGAGCTCTTCGATAATTCAGGCTTTTAATCGAGATATAGAAGATAAT 540
Qy 81 AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
Db 541 GCTCCCTTTCAGAAAGGGGACAGACCCTTCTCACTTAATCTCGGTGTGACCTCCCATATA 600
Qy 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLys 120
Db 601 AACCCGCAAAATATATATATTTTCAGAGCCATCGAACTTGTATCGCAGCTAACCCAAAA 660
Qy 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
Db 661 GAGCCTTTGTATCATTAATTTGATTACGATTTTCAACGAAGATTGATCAATCTACATAGG 720
Qy 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
Db 721 GGACAAAGGCTTGGATATATATCTGGAGAGACTTTCTGCCTGAAATCATACCTACTCTCAGGAG 780
Qy 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
Db 781 ATGTATTTGAATATGTTATGAAATAAACAGCGGCGCTTTTCAGATTAACTTGAGACTC 840
Qy 181 MetGluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheIleAsnLeu 200
Db 841 ATGGAAGCGCTGTCTCTCTCTCACACCGCGCATTCGTTGGTTCCTTTTCATAAATCTT 900
Qy 201 LeuGlyIleIleTyrGlnIleAArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSer 220
Db 901 CTGGGTATTATTATCAGATTAGATGATTACTTGAATTTGAAGAGATTTTCCAAATGTCC 960
Qy 221 SerGluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHis 240
Db 961 AGCGAAAAGGCTTCTGCTGAGGACATTTACAGAGGGAAGTTATCTTTTCCCATCGTCCAC 1020
Qy 241 AlaLeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIle 260
Db 1021 GCCCTTTAACTTCACTAAACGAAAGGTCAAACTGAGCAACACCAATGAAATTTCTAAGAATT 1080
Qy 261 LeuLeuLeuArgThrSerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGluPhe 280
Db 1081 CTCTCTGTGAGGACAAAGTGAAGATATAAATAAAGCTGATTTCAAAATCTGGAATTC 1140
Qy 281 AspThrAsnSerLeuAlaTyrThrLysAsnPheIleAsnGlnLeuValAsnMetIleLys 300
Db 1141 GACACCAATTCATTTGGCCTACACCAAAAATTTTATTAATCAATTAGTGAATATGATATA 1200
Qy 301 AsnAspAsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThrAsn 320
Db 1201 AATGATAATGAAATAAGTATTTTACCTGATTTGGCTTCGCATTTCCGACCCGCCAAT 1260
Qy 321 LeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db 1261 TTACATGACGAATTTGTATATATAATAGACCACTTATCCGAATTTG 1305

RESULT 4

US-10-487-901-363
; Sequence 363, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteris

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; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 363
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-487-901-363
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Alignment Scores:
Pred. No.: 2,548-98 Length: 599
Score: 974.00 Matches: 188
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 97.4% Mismatches: 4
Query Match: 56.6% Indels: 0
DB: 9 Gaps: 0
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US-10-041-018-22 (1-335) x US-10-487-901-363 (1-599)

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QY 1 MetGluAlaLysIleAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGlu 20
DB 19 ATGGAGGCCAACATACATGAGTGCATCATATATGATCTGTTGGTCCAGCCCAATGAA 78
QY 21 SerLeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeu 40
DB 79 AGCTTGATTTCAAAACCTTATAATCACATCCCTTTGAAACCTGGCAAGAACTTTAGACTA 138
QY 41 AsnLeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleVal 60
DB 139 AATTTAATAGTTCAAAATTAACAGAGTTATGAATTTGCCCAAGACAGCTGCCATAGTT 198
QY 61 SerGlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsn 80
DB 199 TGCATAATGTTGAGCTCTTGCTATATTCAGCCTTTTAATCGCATATAGAGTAAT 258
QY 81 AlaProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIle 100
DB 259 GCTCCCTTGAGAAGGGGACAGACCACTTCTCACTTAATCTCGGTGTACCTCCACTATA 318
QY 101 AsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrLys 120
DB 319 AACACCGGAAATATATGTTATTTACAGACCATGCACTTGTATCGCAGTAACCAAAA 378
QY 121 GluProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArg 140
DB 379 GAGCCTTTGTATCATATAATTTGATTACAAATTTCAAGAAAATTTGATCAATCTACATAGG 438
QY 141 GlyGlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGlu 160
DB 439 GGACAAGGCTTGGATATATCTGGAGAGACTTCTGCGCTGAAATCATACCTACTCAGGAG 498
QY 161 MetTyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeu 180
DB 499 ATGTATTTGAATATGGTTATGTAATAAACAGGGCGCTTTTCAGATTAACTGTGAGACTC 558
QY 181 MetGluAlaLeuSerProSerSerHisHisGlyHisSer 193
DB 559 ATGGAAACACTGTCTCTCTCTCCACACCAACCGGGCATTCG 597
```

RESULT 5

```
US-10-369-493-36092
; Sequence 36092, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
```

```
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36092
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-369-493-36092

Alignment Scores:
Pred. No.: 1,668-59 Length: 1044
Score: 629.50 Matches: 127
Percent Similarity: 64.6% Conservative: 63
Best Local Similarity: 43.2% Mismatches: 87
Query Match: 36.6% Indels: 17
DB: 6 Gaps: 6
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US-10-041-018-22 (1-335) x US-10-369-493-36092 (1-1044)

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QY 2 GluAlaLysIleAspGluLeuIleAsnAsnAspProValTrpSerSerGlnAsnGluSer 21
DB 157 CAGTCAAGTCTCGACGGGACAAATAACAAGATGGGAATGTCCCAAGAGATGAGGAG 216
QY 22 LeuIleSerLysProTyrAsnHisIleLeuLeuLysProGlyLysAsnPheArgLeuAsn 41
DB 217 GTGATCATGGTCCGTACGACTACATGCTGCAACACCCGGGGAAGACCTGCGACGGCAG 276
QY 42 LeuIleValGlnIleAsnArgValMetAsnLeuProLysAspGlnLeuAlaIleValSer 61
DB 277 ATGATCAACGCTTTTAACGTATGTTGAAGTGGCCATCTGAGAGCCTTGCCCATCATCAC 336
QY 62 GlnIleValGluLeuLeuHisAsnSerSerLeuLeuIleAspAspIleGluAspAsnAla 81
DB 337 AAAGTAGTGGTATGCTTCATACCCCTTCATTATTGATCGACGACGTCGAAGCAACTCT 396
QY 82 ProLeuArgArgGlyGlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsn 101
DB 397 CTCTCCGGCAGGAAATCCGGTCCGACATAGTCTATGGCACCGCGCAGACGATCAAT 456
QY 102 ThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuValSerGlnLeuThrLysGlu 121
DB 457 TCGGCAAACTAGTCTTACTTCTCCCTCCAGGAGGTCAAAACTG-----AAGAGT 510
QY 122 ProLeuTyrHisAsnLeuIleThrIlePheAsnGluGluLeuIleAsnLeuHisArgGly 141
DB 511 CCGGCA-----GCTATCGACATATACGTCCAGGAGCTGCTGNAATTTACACAGAGG 561
QY 142 GlnGlyLeuAspIleTyrTrpArgAspPheLeuProGluIleIleProThrGlnGluMet 161
DB 562 CAAGCATGATCTGTCTCTGGCGAGACACGCTC-----ACTTGTCCAAGCGAAGATGAA 615
QY 162 TyrLeuAsnMetValMetAsnLysThrGlyLeuPheArgLeuThrLeuArgLeuMet 181
DB 616 TACTTGGAGATGGTGGGCAACAAGACTGGAGGTTTGTTCGGCTAGCTGTAATTTGATG 675
QY 182 GluAlaLeuSerProSerSerHisHisGlyHisSerLeuValProPheIleAsnLeu 201
DB 676 CAAGCT-----GAAAGCAGCACTGGAAGGACTGTGGCCCTGTGTAATGTTTTG 726
QY 202 GlyIleIleTyrGlnIleArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSerSer 221
DB 727 GGACTGGTCTTTCAGATATGCGACGACTATCTCAATTTATCCGACACGACGTATACCCAG 786
QY 222 GluLysGlyPheAlaGluAspIleThrGluGlyLysLeuSerPheProIleValHisAla 241
DB 787 AACAAAGGGCTCTGTGAAGACCTCAAGAGGGCAAAATTTTCCCTCCATTATCCACAGC 846
QY 242 LeuAsnPheThrLysThrLysGlyGlnThrGluGlnHisAsnGluIleLeuArgIleLeu 261
DB 847 ATTCGA-----TCGAACCGGGGAACCATCAGCTCATCAATATCTTC 888
```



```
QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsn 69
DB 284 CTGAAGTTCAGAGGACAGCTACAGATATTATTGAATGACAGAAATGTTGCATAAT 343
QY 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuLeuArgGlyGlnThrThr 89
DB 344 GCAGTTTACTCATGATGATATTGAACAACACTCAAACTCCGAGCTGGCTTCCAGTG 403
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 404 GCCCAGCATCTATGGAATCCCACTGTCATCAATCTCGCAATACGTGATTTCCCTT 463
QY 110 AlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 464 GCGTTTGGAGAAAGTC-----TTAACCTTGTATCACCCA-----GATGAGTGAAG 508
QY 130 IlePheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 509 CTTTTTACCCCGCAGCTTTTGGAACTCCATCAGGGACAAGGCTAGATATTTACTGGAGG 568
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 569 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGCAGAAA 622
QY 170 ThrGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 189
DB 623 ACAGGTGGACTGTTGGATTAGCAGTAGGTCTCATGCAGTTGTC-----TCTGAT 673
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAsp 209
DB 674 TCAAAAGAAGATTAAACCGCTACTTAATACACTTGGGCTCTTTTCCAAATTAGGGAT 733
QY 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
DB 734 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAACAAAGTTTGTGAAGATCTG 793
QY 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
DB 794 ACAGAGGGAAGATTCTCATTTCTACTATTCATGCTATT-----TGG 835
QY 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
DB 836 TCAAGGCTTGAAGACCCAGGTGGAGATATCTTGGCCGACAGAACAGAAACATAGAT 895
QY 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
DB 896 ATAAAAAATACTGTGTACATTATCTTGAG---GATGTAGGTCTTTTCAATACACTCGT 952
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
DB 953 AATACCTTAAAGAGCTT-----GAGCTAAA-----979
QY 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
DB 980 -----GCCATAAACAGATTGATGCACGTGTGGGAACCCCTGAGCTAGTACCTTAGTA 1033
QY 330 AspHisLeuSerGluLeu 335
DB 1034 AAACACTTAAGTAAGATG 1051
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RESULT 8

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US-09-814-353-21762
; Sequence 21762, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-0068
```

```
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21762
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1692
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21762
```

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Alignment Scores:
Pred. No.: 4,27e-54 Length: 1692
Score: 584.00 Matches: 130
Percent Similarity: 57.7% Conservative: 58
Best Local Similarity: 39.9% Mismatches: 106
Query Match: 34.0% Indels: 32
DB: 3 Gaps: 9
```

US-10-041-018-22 (1-335) x US-09-814-353-21762 (1-1692)

```
QY 12 AspProValTrpSerSerGlnAsn-----GluSerLeuIleSerLysProTyrAsnHis 29
DB 249 AATCCAATGGAGAGACACTCAAGAAACAGTCCAAAGAAATTTCTTAGAACCTTATAATAC 308
QY 30 IleLeuLeuLysProGlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgVal 49
DB 309 TTACTTTCATTACAGGTAAACAAGTGAGAACCAACTTTCACAGCATTTAATCATTTGG 368
QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsn 69
DB 369 CTGAAGTTCAGAGGACAAAGCTACAGATATTATTGAAGTCACAGAAATGTTGCATAAT 428
QY 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThr 89
DB 429 GCAGTTTACTCATGATGATATTGAAGACAACTCAAAACTCCGAGCTTCCAGTG 488
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 489 GCCCAGCATCTATGGAATCCCACTGTCATCAATCTGCCAATACGTGATTTCCCTT 548
QY 110 AlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 549 GCGTTTGGAGAAAGTC-----TTAACCTTGTATCACCCA-----GATGAGTGAAG 593
QY 130 IlePheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 594 CTTTTTACCCCGCAGCTTTTGGAACTCCATCAGGGACAAGGCTAGATATTTACTGGAGG 653
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 654 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGCAGAAA 707
QY 170 ThrGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 189
DB 708 ACAGGTGGACTCTTTGGATTAGCAGTAGGTCTCATGCAGTTGTC-----TCTGAT 758
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAsp 209
```

```
Db 759 TACAAGAGGATTTAAACCGCTACTTAATACACTTGGGCTCTTTTCCAAATAGGGAT 818
Qy 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
Db 819 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAACAAAAGTTTTTGTGAAGATCTG 878
Qy 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
Db 879 ACAGAGGGAAGTCTCAATTCCTACTATTTCATGCTATT-----TGG 920
Qy 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuLeuArgThrSerAspLysAsp 269
Db 921 TCAAGGCGCTGAAGACCCAGGTGCAGAAATATCTTGGCCAGAGAACAGAAAACATAGAT 980
Qy 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
Db 981 ATAAAAAATPACTGTGTACATTATCTTGGAG---GATGTAGGTTCTTTTGAATACACTCGT 1037
Qy 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
Db 1038 AATACCTTAAGAGCTT-----GAAGCTAAA----- 1064
Qy 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
Db 1065 -----GCCTATAACAGATTGATGCACGTTGGTGGGAACCTGAGCTAGTAGCTTAGTA 1118
Qy 330 AspHisLeuSerGluLeu 335
Db 1119 AAACACTTAAGTAAGATG 1136

RESULT 9
US-10-041-018-3
; Sequence 3, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080U1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Human
US-10-041-018-3

Alignment Scores:
Pred. No.: 8.15e-54 Length: 2534
Score: 584.00 Matches: 130
Percent Similarity: 57.7% Conservative: 58
Best Local Similarity: 39.9% Mismatches: 106
Query Match: 34.0% Indels: 32
DB: Gaps: 9

US-10-041-018-22 (1-335) x US-10-041-018-3 (1-2534)

Qy 12 AspProValTrpSerSerGlnAsn-----GluSerLeuLysSerLysProTyrAsnHis 29
Db 227 AATCCATGTGAGAGACTCAAGAAACAGTCCAAAGAAATCTTCTAGAACCCCTATAATAC 286
Qy 30 IleLeuLysProGlyLysAsnPheArgLeuAsnLeuValGlnIleAsnArgVal 49
Db 287 TTACTTCAGTTACAGGTAAACAAAGTGCAGAACCACTTTTCACAGGCAATTAATCATGG 346
Qy 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsn 69
Db 347 CTGAAAGTTCCAGAGGCAAGCTACAGATTATTATTGAAGTGCAGAGAAATGTTGCATAAT 406
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```
Qy 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThr 89
Db 407 GCAGTTTACTCATCATGATATTTGAAGACAACTCAAACTCCGACCTGGCTTCCAGTG 466
Qy 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
Db 467 GCCACAGACATCTATGAATCCCATCTGTCAATCTCAATCTGCAATTAACGTATTTCTCT 526
Qy 110 AlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThr 129
Db 527 GGCTTGGAGAAAGTC-----TTAACCTTTGATCACCCA-----GATGCAGTAGAG 571
Qy 130 IlePheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTyrArg 149
Db 572 CTTTTTACCCGCCAGCTTTTGGAACTCCATCAGGACAGCCCTAGATATATTACTGGAGG 631
Qy 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
Db 632 GAT-----AATTACACTTGTCCACTGAAGAAAGATATAAAGCTATGGTGTGCAGAAA 685
Qy 170 ThrGlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 189
Db 686 ACAGGTGGACTGTTGGATTAGCAGTAGGTCTCATGCACTGTGTC-----TCTGAT 736
Qy 190 HisGlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAsp 209
Db 737 TACAAGAGAGATTAAACCGCTACTTTAATACACTTGGGCTCTTTTCCAAATTAGGAT 796
Qy 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
Db 797 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAAAACAAAGTTTTTGTGAAGATCTG 856
Qy 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
Db 857 ACAGAGGGAAGTCTCATTTCTCTACTATTCTGCTATT-----TGG 898
Qy 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
Db 899 TCAAGGCGCTGAAGACCCAGGTGCAGAAATATCTTGGCCAGAGAACAGAAAACATAGAT 958
Qy 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
Db 959 ATAAAAAATPACTGTGTACATTATCTTGAG---GATGTAGGTTCTTTTGAATACACTCGT 1015
Qy 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
Db 1016 AATACCTTAAAGAGCTT-----GAAGCTAAA----- 1042
Qy 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
Db 1043 -----GCCTATAACAGATTGATGCACGTTGGTGGGAACCCCTGAGCTAGTAGCCTTAGTA 1096
Qy 330 AspHisLeuSerGluLeu 335
Db 1097 AAACACTTAAGTAAGATG 1114

RESULT 10
US-09-925-302-171
; Sequence 171, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 171
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-171

Alignment Scores:
Pred. No.: 4,9e-53 Length: 2529
Score: 577.00 Matches: 129
Percent Similarity: 57.4% Conservatives: 58
Best Local Similarity: 39.6% Mismatches: 107
Query Match: 33.5% Indels: 32
DB: 3 Gaps: 9

US-10-041-018-22 (1-335) x US-09-925-302-171 (1-2529)

QY 12 AspProValTrpSerSerGlnAsn-----GluSerLeuIleSerLysProTyrAsnHis 29
DB 215 AATCCAAATGGAGAAGACTCAAGAAACAGTCCAAAGAAATCTCTAGAACCCCTATAAATAC 274
QY 30 IleLeuLeuLysProGlyLysAsnPheArgLeuAsnLeuValGlnIleAsnArgVal 49
DB 275 TTACTTTCAGTTACCAAGTAAACAGTGAAGAACCAAACTTTCAGGCAATTTAATCATGG 334
QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuHisAsn 69
DB 335 CTGAAAGTTCCAGAGGACAAAGCTACAGATTATTATGAAGTGACAGAAATGTTGCATAAT 394
QY 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThr 89
DB 395 GCCAGTTTACTCATCGATGATATTGAAGACAACTCAAAACCTCCGACGTGGCTTTCAGTG 454
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 455 GCCCAGCATCTATGGAATCCATCTGTCAATCTGCAATTTCCCAATTTACGTATTTCCTT 514
QY 110 AlaMetGlnLeuValSerGlnLeuThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 515 GCGTTGGAGAAAGTC-----TTAACCCCTTGATCACCCA-----GATGCAAGTGAAG 559
QY 130 IlePheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 560 CTTTATACCCGCCAGCTTTTGGAACTCCATCAGGACCAAGGCTAGATATTACTGGAGG 619
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 620 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGTGCAGAAA 673
QY 170 ThrGlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerHis 189
DB 674 ACAGGTGGAAGTCTGTGGATTAGCAGTAGCTCTCATGCACTTGTC-----TCTGAT 724
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuGlyIleTyrGlnIleArgAsp 209
DB 725 TCAAGAAGAAGATTAAACCGCTACTTAATACACTTGGGCTCTTTTCCAAATTTAGGAT 784
QY 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
DB 785 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAGAACAAAGTTTGTGTGAAGATCTG 844
QY 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
DB 845 ACAGAGGGAAGAGTTCTCATTTCTACTATTCTATGCTATT-----TGG 886
QY 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
DB 887 TCAAGYCTGAAGACACCCAGGTGCAAGATATCTCCGACAGAAACAAACATAGAT 946
QY 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
DB 947 ATAAAAAATACTGTGTACATTATCTTGAG---GATGTAGGTTCTTTTGAATACACTCGT 1003
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
```

```
Db 1004 AATACCCTTAAAGAGCTT-----GAAGCTAAA----- 1030
QY 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
DB 1031 -----GCCTATAAACAGATTGATGACGTGGTGGGAACCCCTAGCTAGCTTAGTA 1084
QY 330 AspHisLeuSerGluLeu 335
DB 1085 AAACACTTAAGTAAGATG 1102

RESULT 11
US-09-925-302-171
; Sequence 171, Application US/09925302
; Publication NO. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 171
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-171

Alignment Scores:
Pred. No.: 4,9e-53 Length: 2529
Score: 577.00 Matches: 129
Percent Similarity: 57.4% Conservatives: 58
Best Local Similarity: 39.6% Mismatches: 107
Query Match: 33.5% Indels: 32
DB: 3 Gaps: 9

US-10-041-018-22 (1-335) x US-09-925-302-171 (1-2529)

QY 12 AspProValTrpSerSerGlnAsn-----GluSerLeuIleSerLysProTyrAsnHis 29
DB 215 AATCCAAATGGAGAAGACTCAAGAAACAGTCCAAAGAAATCTCTAGAACCCCTATAAATAC 274
QY 30 IleLeuLeuLysProGlyLysAsnPheArgLeuAsnLeuValGlnIleAsnArgVal 49
DB 275 TTACTTTCAGTTACCAAGTAAACAGTGAAGAACCAAACTTTCAGGCAATTTAATCATGG 334
QY 50 MetAsnLeuProLysAspGlnLeuAlaIleValSerGlnIleValGluLeuHisAsn 69
DB 335 CTGAAAGTTCCAGAGGACAAAGCTACAGATTATTATGAAGTGACAGAAATGTTGCATAAT 394
QY 70 SerSerLeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThr 89
DB 395 GCCAGTTTACTCATCGATGATATTGAAGACAACTCAAAACCTCCGACGTGGCTTTCAGTG 454
QY 90 SerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArg 109
DB 455 GCCCAGCATCTATGGAATCCATCTGTCAATCTGCAATTTCCCAATTTACGTATTTCCTT 514
QY 110 AlaMetGlnLeuValSerGlnLeuThrLysGluProLeuTyrHisAsnLeuIleThr 129
DB 515 GCGTTGGAGAAAGTC-----TTAACCCCTTGATCACCCA-----GATGCAAGTGAAG 559
QY 130 IlePheAsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArg 149
DB 560 CTTTATACCCGCCAGCTTTTGGAACTCCATCAGGACCAAGGCTAGATATTACTGGAGG 619
QY 150 AspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLys 169
DB 620 GAT-----AATTACACTTGTCCCACTGAAGAAGATATAAAGCTATGCTGTGCAGAAA 673
QY 170 ThrGlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerHis 189
DB 674 ACAGGTGGAAGTCTGTGGATTAGCAGTAGCTCTCATGCACTTGTC-----TCTGAT 724
QY 190 HisGlyHisSerLeuValProPheIleAsnLeuGlyIleTyrGlnIleArgAsp 209
DB 725 TCAAGAAGAAGATTAAACCGCTACTTAATACACTTGGGCTCTTTTCCAAATTTAGGAT 784
QY 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
DB 785 GATTATGCTAATCTACACTCCAAAGAAATATAGTGAAGAACAAAGTTTGTGTGAAGATCTG 844
QY 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
DB 845 ACAGAGGGAAGAGTTCTCATTTCTACTATTCTATGCTATT-----TGG 886
QY 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
DB 887 TCAAGYCTGAAGACACCCAGGTGCAAGATATCTCCGACAGAAACAAACATAGAT 946
QY 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
DB 947 ATAAAAAATACTGTGTACATTATCTTGAG---GATGTAGGTTCTTTTGAATACACTCGT 1003
QY 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
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Db 620 GAT-----AATTACACTGTCCCACTGAAGAAGATATAAAGCTATGCTGCAGAAA 673
Qy 170 ThrGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerHis 189
Db 674 ACAGGTGGAGTGTGGATTAGCAGTAGGTCTCATGCAGTTGTC-----TCTGAT 724
Qy 190 HisGlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAsp 209
Db 725 TACAAGAAGATTAAACCGCTACTTAATACACTTGGGCTCTTTTCCAAATAGGAT 784
Qy 210 AspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIle 229
Db 785 GATTATGCTAATCTACACTCCAAAGATATAGTGAAACAAAAGTTTCTGTGAAGATCTG 844
Qy 230 ThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGly 249
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Qy 250 GlnThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAsp 269
Db 887 TCAAGGYCTGAAGACCCAGGTGCAGAAATATCTTGGCCAGAGACAGAAAACATAGAT 946
Qy 270 IleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLys 289
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Qy 290 AsnPheIleAsnGlnLeuValAsnMetIleLysAsnAspAsnGluAsnLysTyrLeuPro 309
Db 1004 AATACCCCTTAAGAGCTT-----GAAAGCTAAA-----1030
Qy 310 AspLeuAlaSerHisSerAspThrAlaThrAsnLeuHisAspGluLeuLeuTyrIleIle 329
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Qy 330 AspHisLeuSerGluLeu 335
Db 1085 AAACACTTAAGTAAGATG 1102

RESULT 12
US-11-097-143-9632
; Sequence 9632, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9632
; LENGTH: 2210
; TYPE: DNA
; ORGANISM: DROSOPHILA
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Pred. No.: 1,29e-49 Length: 2210
Score: 545.50 Matches: 123
Percent Similarity: 56.0% Conservative: 55
Best Local Similarity: 38.7% Mismatches: 113
Query Match: 31.7% Indels: 27
Db: 10 Gaps: 7

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Qy 12 AspProValTyrSerSerGlnAsnGluSerLeuIleSerLysProTyrAsnHisIleLeu 31
Db 332 GATAAATCAACGCAAAAGGAGCAGGATGAGATTCTGCTGCAGCCCTTTACATACATAAA 391
Qy 32 LeuLysProGlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgValMetAsn 51
Db 392 CAGATTCTCTGGCAAGCAATTCGCTCTGAGTTGGCCTTGGCCTTCAATCACTGCTGCTC 451
Qy 52 LeuProLysAspGlnLeuAlaIleValSerGlnIleValGlnLeuLeuLeuHisAsnSer 71
Db 452 ATACCCGGCGCAAAAGTTGGCGCAGATCGGAGACATTTGTCAGATGCTGCACAAATTCAGT 511
Qy 72 LeuLeuIleAspAspIleGluAspAsnAlaProLeuArgArgGlyGlnThrThrSerHis 91
Db 512 TTGCTCATTTGATGATATTGAGACAAATTCGATCCTTCGCAGAGGTGTGCCGTGGCGCAT 571
Qy 92 LeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMet 111
Db 572 TCCATCTACGGCTGGCCAGCACCATAAATCGGCCAACTATGCACCTCTTTCTGGCGCTG 631
Qy 112 GlnLeuValSerGlnLeuThrLysGluProLeuTyrHisAsnLeuIleThrIlePhe 131
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Qy 132 AsnGluGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAspPhe 151
Db 677 ACCGACAAATTTGCGAGCTGCACCGTGGACAGGCATGGAGATCTATTTCGGCGCAGC 736
Qy 152 LeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThrGly 171
Db 737 TTC-----ACGTGTCCATCCGAGTCGGATTACAAGCTGATGACTGTGCGCAAACTGGC 790
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Db 791 GGCCTCTTTTATGCTGGCCATTCGCCCTTATGCACTGTTCAGCTCCCAAGAGGAGCTAT 850
Qy 192 HisSerLeuValProPheIleAsnLeuLeuGlyIleIleTyrGlnIleArgAspTyr 211
Db 851 TCGAAGTTGACGGCT-----ATATTGGGCTGTACTTTTTCAGATACCGCAGCTAT 901
Qy 212 LeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThrGlu 231
Db 902 TGCAATCTGAGTCTGAAAGAGTACACGAGAGAACAGAGCTTCGCCGAGGACTTTCACCGAG 961
Qy 232 GlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGlnThr 251
Db 962 GGCAGGTTCGGCTTCCCGGTAAATCCATGCGGTTTCGCCACCACCAAAAG-----1006
Qy 252 GluGlnHisAsnGluIleLeuArgIleLeuLeuArgThrSerAspLysAspIleLys 271
Db 1007 ---CAGGATAACAGGTTCTACACATATTACGCCAGCGGCAGCAGCATTTAGGTCAAG 1063
Qy 272 LeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsnPhe 291
Db 1064 AAGTACTGTCATCACCTTTGTTGAA---AAGCTGGCAGCTTTTCAGTATATACACCAAGGTT 1120
Qy 292 IleAsnGlnLeuValAsnMetIleLysAsnAsp-----AsnGluAsnLysTyr 307
Db 1121 CTGGAGTCTGCTCGACGACGAGGCTCGTTCGGAGGTGGCTCGTTTGGGTAGCAATCCGTAC 1180
Qy 308 LeuProAspLeuAlaSerHis-----SerAspThrAlaThr 319
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Db 494 GCTTCATTGCT-GTAGGCTCTTTCCACCTCACCACCAACCACTCCAGTTCAGACAGATT 552
Qy 74 -----IleAspAspIleGluAspAsnAlaProLeuArgGly 86
Db 553 GACATTTGTGTAGCGCAGATATCGAGACTACTCCAACTCCGCGCGGC 612
Qy 87 GlnThrThrSerHisLeuIlePheGlyValProSerThrIleAsnThrAlaAsnTyrMet 106
Db 613 TTCCTCTGCGCAGACAGATCTTCGGCATTCGGCATTCGGCAGACAATCACTCTGCTAACTACGCC 672
Qy 107 TyrPheArgAlaMetGlnLeuValSerGlnLeuThrThrLysGluProLeuTyrHisAsn 126
Db 673 TACTTCCAGCAGACAGAGGCTCTGAAATTCGGCAGATCGGAG-----AAA 720
Qy 127 LeuIleThrIlePheAsnGluLeuIleAsnLeuHisArgGlyGlnGlyLeuAspIle 146
Db 721 GCCTTACGTATCTTTACAGAGGAGCTTCTCGGCTGCACAGAGCCAGGAATGGATCTC 780
Qy 147 TyrTrpArgAspPheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetVal 166
Db 781 TACTGGAGGATTCCTTC-----ACCTGCCAGTGAAGAGGAGTACTTGGACATGGTG 834
Qy 167 MetAsnLysThrGlyGlyLeuPheArgLeuThrLeuArgLeuMet----- 181
Db 835 GCAACAAGACGGCGGGCTTTTTCGGCTCGCCATTAAAGCTTATTAGTTTGGAAAGTGAC 894
Qy 182 -----GluAlaLeuSerPro 186
Db 895 GTTGATGAGTTCGTGGCGCTCTTGAGTTTCTTCATTATTTTAGACAAGAGCTGAACAGA 954
Qy 187 SerSerHisGlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGln 206
Db 955 CTTCATTACGG-CCGAGGACTGGTCCCTAGTAGGACCTGCTAGGTATATCTTCAG 1013
Qy 207 IleArgAspAspTyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAla 226
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Qy 227 GluAspIleThrGluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLys 246
Db 1074 GAGGACATACAGAGGCAAGTCTCTACCCGATGTCATATGATATTCGAAGTAGCAGT 1133
Qy 247 ThrLysGly---GlnThrGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThr 265
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Qy 266 SerAspLysAspIleLysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeu 285
Db 1194 GAGGACGAAGCGCTCAAGAAATATATCTATTTCAGATCCTTGAG---AAGACAGGCGAGTTT 1250
Qy 286 AlaTyrThrLysAsnPheIleAsnGlnLeu 295
Db 1251 GAGTTTACGAGGCGAGAGTTTGAGGGATTG 1280
RESULT 15
; Sequence 14, Application US/10001192A
; PUBLICATION NO. US20040091958A1
; GENERAL INFORMATION:
; APPLICANT: Oeljen, Albert
; APPLICANT: Verdoes, Jan
; APPLICANT: Wery, Jan
; TITLE OF INVENTION: IMPROVED METHODS FOR TRANSFORMING
; TITLE OF INVENTION: PHAFIA STRAINS, TRANSFORMED PHAFIA STRAINS SO OBTAINED AND
; FILE OF INVENTION: RECOMBINANT DNA IN SAID METHODS
; FILE REFERENCE: 24615-20104.01
; CURRENT APPLICATION NUMBER: US/10/001,192A
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: EP 95203620.0
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: EP96200943.7
; PRIOR FILING DATE: 1996-04-11
; NUMBER OF SEQ ID NOS: 57
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; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1212)
US-10-001-192A-14
Alignment Scores:
Pred. No.: 6,85e-49 Length: 1882
Score: 538.00 Matches: 117
Percent Similarity: 52.1% Conservative: 79
Best Local Similarity: 31.1% Mismatches: 110
Query Match: 31.3% Indels: 70
DB: 7 Gaps: 7
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Qy 15 TrpSerSerGlnAsnGluSerLeuIleSerLysProTyrAsnHisIleLeuLeuLysPro 34
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Qy 35 GlyLysAsnPheArgLeuAsnLeuIleValGlnIleAsnArgValMetAsnLeuProLys 54
Db 181 GGAAGAATAATTCGATCACAACATCATCGAGGCTTCACTATTGGTTGGATGTCAGAG 240
Qy 55 AspGlnLeuAlaIleValSerGlnIleValGluLeuLeuHisAsnSerSerLeuLeu 74
Db 241 GAGGATCTCGAGGTCATCCAGAACGTTGTGGCATGCTACATACCTAGCTTATTATG 300
Qy 75 AspAspIleGluAspAsnAlaProLeuArgGlyGlnThrThrSerHisLeuIlePhe 94
Db 301 GAGGATGTGGAGGATTCATCGGTCCTCAGGCGTGGTGGCTGTGGCCCATCTAATTAC 360
Qy 95 GlyValProSerThrIleAsnThrAlaAsnTyrMetTyrPheArgAlaMetGlnLeuVal 114
Db 361 GGGATTCGGCAGACAATAACACTGCAAACTAGCTACTTCTTGGCTTATCAAGAGATC 420
Qy 114 ----- 114
Db 421 TTCAAGCTTCGCCCAACACCGATACCATCGCTGTAATTCCTCTCATCTGCTTCGCTT 480
Qy 114 ----- 114
Db 481 CAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
Qy 115 -----SerGlnLeuThrThrLysGluProLeuTyrHisAsnLeuIleThrIle 130
Db 541 TCAACTCTTAATTCGAGATTCGGTTCGAAAGATACGTAT-----CTTGATAAGTG 594
Qy 131 PheAsnGluGluLeuLeuAsnLeuHisArgGlyGlnGlyLeuAspIleTyrTrpArgAsp 150
Db 595 ATCAGACAGCAGATGCTTCCCTCCATAGAGGGCAAGGCTGGAGCTATTCTGAGAGAT 654
Qy 151 PheLeuProGluIleIleProThrGlnGluMetTyrLeuAsnMetValMetAsnLysThr 170
Db 655 AGTCTG-----ACGTGCTCTAGCAGAGGAATATGTGAAATGGTCTTTGGAAAGACG 708
Qy 171 GlyGlyLeuPheArgLeuThrLeuArgLeuMetGluAlaLeuSerProSerSerHis 190
Db 709 GAGGTTTGTTCGTATAGCGGTGAGATGATGATGCA-----AAGTCAGATGT 759
Qy 191 GlyHisSerLeuValProPheIleAsnLeuGlyIleIleTyrGlnIleArgAsp 210
Db 760 GACATAGACTTGTTCAGCTTGTCAACTGATCTCAATATATCTTCCAGATCAGGATGAC 819
Qy 211 TyrLeuAsnLeuLysAspPheGlnMetSerSerGluLysGlyPheAlaGluAspIleThr 230
Db 820 TATATGAACCTTCAGTCTCTCTAGTATGCCCAATAAAGAAATTTTCAGAGGACCTCACA 879
Qy 231 GluGlyLysLeuSerPheProIleValHisAlaLeuAsnPheThrLysThrLysGlyGln 250
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Db      880 GAAGGAAATTCAGTTTCCCACTCCCACTCGATTCAGCCCAACCCCTCATCG----- 933
Qy      251 ThrGluGlnHisAsnGluIleLeuArgIleLeuLeuLeuArgThrSerAspLysAspIle 270
Db      934 -----AGACTCGTCATCAATACGTTGCAGAGAATAATCGACCTCTCTGAGATC 981
Qy      271 LysLeuLysLeuIleGlnIleLeuGluPheAspThrAsnSerLeuAlaTyrThrLysAsn 290
Db      982 CTTCAACCACTGTGTAAACTACATGCGCACAGAAACCCACTCATTCGAATATATCTCAGGAA 1041
Qy      291 PheIleAsnGlnLeuValAsnMetIleLysAsnAsp----- 302
Db      1042 GTCTCTCAACACCTTGTCAAGTGCACCTCGAGAGAACTAGGAAGGCTTCAAGGAGAGTTC 1101
Qy      303 -----AsnGluAsnLysTyrLeuProAspLeuAlaSerHisSerAspThrAlaThr 319
Db      1102 GCAGAGAGCTAACTCAAGGATGGATCTTGGAGACGTAGATTTCGAAGGAAGAACGGGGAAG 1161
Qy      320 AsnLeuHisAspGluLeuLeuTyrIleIleAspHisLeuSerGluLeu 335
Db      1162 AACGTC-----AAATTGGAAGCGATCTCTGAAAAAAGCTAGCCGATATC 1203

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Search completed: February 16, 2006, 10:49:52
Job time : 733.562 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 05:56:03 ; Search time 271.703 Seconds
(without alignments)
10264.856 Million cell updates/sec

Title: US-10-041-018-1

Perfect score: 1569

Sequence: 1 aatattacatatagatag.....aatcgcggttaattcgga 1569

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
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- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1005	64.1	1005	2	US-08-761-344-1
3	114	7.3	903	2	US-08-469-665-1
4	114	7.3	903	2	US-09-038-596-1
5	114	7.3	903	6	PCT-US95-00421-1
6	70.6	4.5	1882	3	US-09-091-725-14
7	65	4.1	498	3	US-09-248-796A-3882
8	52.6	3.4	832	3	US-09-621-976-2813
9	49.8	3.2	1141	3	US-09-806-708B-22
10	48.2	3.1	1664976	3	US-08-916-421B-1
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22	41.6	2.7	385136	3	US-09-949-016-16073
23	41.2	2.6	19438	3	US-09-949-016-12699
24	41	2.6	765	3	US-09-601-198-160

Sequence 1, Appli
Sequence 1, Appli
Sequence 14209, A
Sequence 13614, A
Sequence 16600, A
Sequence 171661, A
Sequence 171662, A
Sequence 2, Appli
Sequence 4, Appli
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Sequence 8427, Ap
Sequence 11614, A
Sequence 179, App
Sequence 573, App
Sequence 720, App
Sequence 12053, A
Sequence 12721, A
Sequence 15692, A

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26 40.8 2.6 1956 3 US-09-351-794A-1
27 40.6 2.6 83210 3 US-09-949-016-14209
28 40.6 2.6 183202 3 US-09-949-016-13614
29 40.6 2.6 298336 3 US-09-949-016-16600
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32 40.2 2.6 601 3 US-08-705-377-2
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37 40 2.5 993 2 US-09-053-068-4
38 39.8 2.5 687 3 US-09-248-796A-8427
39 39.8 2.5 6388 3 US-09-573-080A-179
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42 39.6 2.5 52289 3 US-09-949-016-12053
43 39.4 2.5 87352 3 US-09-949-016-12721
44 39.4 2.5 87352 3 US-09-949-016-12721
45 39.4 2.5 87352 3 US-09-949-016-15692

ALIGNMENTS

RESULT 1

US-08-761-344-3
; Sequence 3, Application US/08761344
; Patent No. 5912154
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yu
; APPLICANT: Ferro-No. 5912154ick, Susan
; TITLE OF INVENTION: GERANYLGERANYL DIPHOSPHATE SYNTHASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,344
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 30,020
; REFERENCE/DOCKET NUMBER: 3161-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/862-0223
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-761-344-3

Query Match 100.0%; Score 1569; DB 2; Length 1569;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 ATTATAGTGGTATCCAAAGCTTCCACCGTTCCAGCATAGCAGAAATTTACGTGTTTTGCGAT 120
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Db
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RESULT 2
US-08-761-344-1
; Sequence 1, Application US/08761344
; Patent No. 5912154
; GENERAL INFORMATION:
; APPLICANT: Ferro-No. 5912154ick, Susan
; APPLICANT: Jiang, Yu
; TITLE OF INVENTION: GERANYLGERANYL DIPHOSPHATE SYNTHASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,344
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 30,020
; REFERENCE/DOCKET NUMBER: 3161-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/862-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1005 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1005
; US-08-761-344-1

Query Match      64.1%; Score 1005; DB 2; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.9e-246; Indels 0; Gaps 0;
Matches 1005; Conservative 0; Mismatches 0;

Qy 301 ATGAGGCCAAGATAGATGAGTCAATTAATGATCCTGTTGGTCCAGCCAAATGAA 360
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Db 181 TCGCAAAATGTTGAGCTTTTCATTAATCCAGCCTTTTAAATCGACGATATAGAAGATAAT 240

Qy 541 GCTCCCTTGAGAGGGGACAGACCACTTCTCACTTAATCTTCGGTGTACCTCCTCATATA 600
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Db 301 AACACCGCAATATATATGTTTTCAGAGCCTGCACTGTTGCGAGCTTAACCAACAAA 360

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Db 361 GAGCCTTTGATCATAATTTGATTAACGATTTTCAACGAAGATTTGATCAATCTACATAGG 420

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Db 421 GGACAGGCTTGGATATATATCTGAGAGACTTTCTGCTGAATCATACCTACTCAGGAG 480

Qy 781 ATGATTTGAATATGTTTATGAATAAACAAGGGGCGCTTTTCAGATTAAGCTTGAGACTC 840
Db 481 ATGATTTGAATATGTTTATGAATAAACAAGGGGCGCTTTTCAGATTAAGCTTGAGACTC 540

Qy 841 ATGGAAGCGCTGTCCTCTCTCACCACCGGCGCATTCGTTGGTTCCTTTTCAATAATCTT 900
Db 541 ATGGAAGCGCTGTCCTCTCTCACCACCGGCGCATTCGTTGGTTCCTTTTCAATAATCTT 600

Qy 901 CTGGGTATTTATCAGATTAGAGATGATTAATTTGAATTTGAAGATTTCCAAATGTCC 960
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Qy 1021 GCCCTTAACTTCACTAAAACGAAGGTCAAACTGAGCAACAATGAAATTTCTAAGAAAT 1080
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Qy 1141 GACACCAATTCATTTGGCCTACACCAAAATTTTATTAATCAATTAGTGAATATGATAAA 1200
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RESULT 3
US-08-469-665-1
; Sequence 1, Application US/08469665
; Patent No. 5786193
; GENERAL INFORMATION:
; APPLICANT: GREENE, ET AL.
; TITLE OF INVENTION: Human Geranylgeranyl Pyrophosphate Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,665
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00421
; FILING DATE: 11 JAN 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-377
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
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; US-08-469-665-1

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Query Match      7.3%; Score 114; DB 2; Length 903;
Best Local Similarity 52.1%; Pred. No. 2.9e-19;
Matches 348; Conservative 0; Mismatches 290; Indels 30; Gaps 3;

Qy 359 AAAGCTTGATTTCCAAACCTTATAATCACATCTTTTGAACCTGGCAAGACTTTAGAC 418
Db 26 AAAGAAATCTTTAGAACCTTATAATATCTTACGTTACCAGGTAACAGATGAGAA 85

Qy 419 TAAATTTAATAGTTCAAATTTAACAAGATTTATGAATTTGCCCAAGACCAAGCTGGCCATAG 478
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Qy 479 TTTTCGCAAAATTTGTAGCTCTTTCGATTAATTCAGACCTTTTAAATCGACGATATAGAAGATA 538
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Qy 539 ATGCTCCCTTGAGAAGGGGACAGACCACTTCTCACTTAACTTCGGTGTACCTCCACTA 598
Db 206 ACTCAAAACTCCGACGCTGGCTTTCCAGTGGCCACAGCATCTATGGAAATCCCATCTGTCA 265

Qy 599 TAAACACCGCAAAATTTATGATTTTTCAGAGCCCATGCAACTTTGTATCGCAGCTAACCAAA 658

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Best Local Similarity 48.1%; Pred. No. 0.25;
Matches 137; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 368 TTTCAAAACCTTATATCAATCATCTCTTTTGAACCTGGCGAAGAACTTTAGACTAAATTTAA 427
Db 688622 TATATAACCGTCAAAACATCTTCTATTTCCTGGAGGAAAGAAATTAGCCCATATTTAA 688681

QY 428 TAGTTCAATTAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATAGTTTCGCAAA 487
Db 688682 CTGTAGTAACTTATATGTTTGAAGAAGACGATATGAGGAGGTTTTCAGCGCGCTGCTG 688741

QY 488 TTGTTGAGCTCTTGCAATATCCAGCTTTTAAATCGACGATATAGAAGATAATGCTCCCT 547
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RESULT 11
US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
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Query Match          3.1%; Score 48.2; DB 3; Length 1664976;
Best Local Similarity 48.1%; Pred. No. 0.25;
Matches 137; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 368 TTTCAAAACTTATATCATCATCTTTTGAAACCTGGCAAGAACTTTAGACTAAATTTAA 427
Db 688622 TATATAACGGTCAAAACATCTTCTATTTGCTGGAGAAAGAAATTAGGCCATATTTAA 688681

QY 428 TAGTTCAAAATTAACAGAGTTATGAATTTGCCAAAGACCAGCTGGCCATAGTTTTCGCAAA 487
Db 688682 CTGTAGTAACTTATATTTGAAGAAAGACGATATTGAGGAGGTTTTCGCCAGCGCTGCTG 688741

QY 488 TTGTTGAGCTCTTGCAATAATTCAGCGCTTTTAAATCGACGATATAGAAATATGCTCCCT 547
Db 688742 CAGTAGAGTTAAATTCACAACTACACCTTAATACATGATGACATTATGGACAAATGATG 688801

QY 548 TGAGAGGGGACAGACACCTTCTCACTTAATCTTGGTGTTACCTCCACTATAAACACCG 607
Db 688802 AGAGGAGAGGAAACCAACAGTTCATGTTCTATGAGAGGCAATGGCTATCTTAGCTG 688861

QY 608 CAAATATATGTTATTTTCAGAGCGCATCAACTTGTATCGCAGCTAA 652
Db 688862 GAGATTTATATATGCTAAAGCTTTTGAAGCAGTTTCAAGATAAA 688906

RESULT 12
US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 661762
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)..(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)..(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
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; LOCATION: 154217
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; LOCATION: (164037)..(164136)
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; NAME/KEY: exon
; LOCATION: (118288)..(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)..(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)..(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)..(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)..(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)..(386186)
; OTHER INFORMATION: intron 11:exon 12
; US-10-027-983-11
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Best Local Similarity 50.0%; Pred. No. 0.86;
Matches 113; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Query Match	2.8%	Score 44.6;	DB 3;	Length 50000;
Best Local Similarity	45.9%;			
Pred. NO.	0.6;			
Matches 152;	Conservative	0;	Mismatches 179;	Indels 0;
Gaps	0;			

Query Match	2.8%;	Score 44.6;	DB 3;	Length 50000;
Best Local Similarity	45.9%;	Pred. No. 0.6;		
Matches 152;	Conservative 0;	Mismatches 179;	Indels 0;	Gaps 0;
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Qy	1156	GCCTACACCAAAAAATTTTATTAAATCAATTTAGTGAATATGATAAAAAATGATAATGAAAAAT	1215	
Db	25804	GAAATTAAGAAAAATAACTATATTTCTAGATGATATATAAAAAATAATATTTAANA	25745	
Qy	1216	AAGTATTTACCTGATTTGGCTTCGCATTCGGACACCGCCACCAATTTTACATGACGAATTTG	1275	
Db	25744	ATATCTAGAATAAGAAATTTAAATAAAATAAATAATAGATAATATTAACAAAAATCAAAATTA	25685	
Qy	1276	TTATATATAATAGACCACTTATCCGAATTTGTGAATAAATTTGATCAATCAAAATTAGTGGTA	1335	
Db	25684	TGGGATTTATTTAAGCAATATTTTCAGTGGGAAAAATGTAAACACCTATATAATTTATAAT	25625	
Qy	1336	GGAAAGTAGTCAGAAATAAAGCTTCTCTCCCTCTTTTCGCATCTATACATACGATTTTC	1395	
Db	25624	GATAAAAAATTAACAATAACTATTTTGATTAATAATAGTTTTTTTTTCATATGCTAACATTTTA	25565	
Qy	1396	ATATATACGTTTTTCATTTGTCATCATCTTTTGGAT	1426	
Db	25564	GTATATTTTTCTAACTTAAATTAATTTACTTCATCAT	25534	

RESULT 15

Query Match	2.7%	Score 43;	DB 3;	Length 1055;
Best Local Similarity	21.2%;	Pred. No. 0.39;		
Matches 126;	Conservative 157;	Mismatches 299;	Indels 12;	Gaps 2;

Query Match 2.7%; Score 43; DB 3; Length 1055;
Best Local Similarity 21.2%; Pred. No. 0.39;
Matches 126; Conservative 157; Mismatches 299; Indels 12; Gaps 2;
QY 886 CCTTTCATAAAATCTCTCGGTATATTATACAGATTAGAGATGATTACTTGAATTTGAAA 945
634 CATNTTWARATNTNTTFRAGGAATNTKTGTTSTTTAGCTMYTGTATGCGNNNNNNNNNNCMTASC 575
Db

